2

ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET

WASHINGTON

USA

COUNTRY:

STREET: 51 UNITY CITY: SEATTLE STATE: WASHING

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES.

FITLE OF INVENTION:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

98101

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240
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Pred. No. 2.4e-179;
0; Mismatches 2;
           OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple S
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140..796
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83..139
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STRANDEDNESS: single
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LOCATION: 83.
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APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE Sequence 1, Application US/08240124 Patent No. 5516658 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08453943
Patent No. 7538644
GENERAL INFORMATION:
APPLICANT: DERCHANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION:
TITLE OF INVENTION:
TOMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: 51 UNIVERSITY STREET
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MEDIUM TYPE: Floppy disk
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CITY: SE
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Pred. No. 2.4e-179;
); Mismatches 2;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILLIN DATE: 20-A0C-1993
ATORNEY ABORN INFORMATION:
NAME: SEESE, ŘATHRYN A.
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAX-1995
GLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                            APPLICATION NUMBER: US 08/240,124 FILING DATE: 09-MAY-1994 APPLICATION NUMBER: US 08/161,132 FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA:
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FILING DATE: 30-AUG-1993
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(206) 233-0644
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al Similarity 99.8%;
919; Conservative
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Best Local Similarity
Matches 919; Conserv
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US-08-453-943-1
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: July 13, 2002 10.44.50 . Search time 65 87 Searchs
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Run on: July 13, 2002, 10:44:50; Search time 65.87 Seconds (without alignments) 625.061 Million cell updates/sec Title: US-09-733-756-2 Perfect score: 1301 NAAAPLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238

Sequence: I MAAAPLLLLLLUPVPVBLLPL.....REHLF
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 56222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 56
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum DB seq length: 20000000000

562222

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries
Listing first 45 summaries
SPTREMBL\_19:\*
1: SP\_archea:\*
2: SP\_bacteria:\*
3: SP\_bacteria:\*
4: SP\_human:\*
4: SP\_human:\*
5: SP\_human:\*
6: SP\_human:\*
7: SP\_human:\*
6: SP\_human:\*
7: SP\_human:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:

SUMMARIES

0923q rattus norv 098tz1 gallus gall 09ptd0 ctenophorus 09czs8 mus musculu 093431 brachydanio 09wuch rattus norv 09wuch rattus norv 09ptd1 ctenophorus 042304 brachydanio 090zg7 brachydanio 090zg7 brachydanio Q90yc5 brachydanio 09puj4 gallus gall 09v4el drosophila 09pt69 xenopus lae Description 09PTD1 042304 09CRL3 090ZG7 090Z31 09PT69 09PU4 Q90YC5 Q923G4 Q98TZ1 Q9PTD0 Q9CZS8 Q9C331 Q9D7K8 Π 13 13 13 13 13 DB Query Match Length 1118 202 88 202 205 102 102 93 80 80 42 42 70 331 333 652 32.6 31.2 31.2 28.7 28.7 28.7 28.7 26.0 20.6 19.0 115.0 112.6 112.5 111.1 373 367 338 268.5 247.5 208 178 166.5 165.5 Result Š.

044516 caenorhabdi 09u474 caenorhabdi 090232 brachydanio 090233 brachydanio 074823 schizosacch	09v9y3 drosophila 09ykq0 human immun 09nq99 homo sapien 09nnrn2 homo sapien	Ogates House musculu (Oglav) Runs musculu (Oglav) Runs musculu (Oglav) Runs musculu (Oglav) Runs Sapien (Oglav) Runs (Oglav) Runs Musculu (Oglav) Runs Muscu	09r262 mus musculu 09217 mus musculu 016783 caenorhabdi 09ykq4 human immun 017657 caenorhabdi		V991D1 rattes holv Q99p6 drosophila Q9dif1 human polio Q9bc3 homo sapien Q13648 homo sapien
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## ALIGNMENTS

MEDLINE-21412237; PubMed=11520665;
MEDLINE-21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
Miedetion of ephrin-A3 and novel genes specific to the midbrainMHB in embryonic zebrafish by ordered differential display.";
Mech. Dev. 107:83-96(2001).

EMBL; AB051678; BAB55891.1; -.

SEQUENCE 219 AA; 25146 MW; 7191927E03F8EA01 CRC64; 54 IYCPHYNSS------QRGIAEQYVLYMVSYRGYRTCDPQLGFKRWECNRPHAPHAPI 104 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180 61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120 18; Gaps 1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60 EPHRIN.43.

Brachydanio rerio (Zebrafish) (Zebra danio).

Brachydanio rerio (Zebrafish) (Zebra danio).

Brachydanio metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio. Query Match 55.9%; Score 727; DB 13; Length 219; Best Local Similarity 61.9%; Pred. No. 1.4e-67; Matches 140; Conservative 25; Mismatches 43; Indels 11 Last sequence update)
Last annotation update) 219 AA Created) PRT; 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, PRELIMINARY; EPHRIN-A3 Q90YC5; RESULT 090YC5 pp ò а ò

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91E2716FF91353F9 CRC64;

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202 AA; 22624 MW;
                 PROSITE; PS01299; EPHRIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Menzel P., Valencia F., God ment P., Dodelet V.C., Pasquale E.B.; "Ephrin A6, a new ligand for EphA receptors in the developing visual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A.,
Jimenez E., Varas A., Zapata A.G.;
"Expression and function of the Eph A receptors and their ligands
ephrins A in the rat thymus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ARV045577; AAK92219.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.0%; Score 586; DB 11; Length 118; 72.4%; Pred. No. 3e-53; tive 3; Mismatches 5; Indels 34
                                                                 181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAV 226
                                                                                                System.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317286; ARK00944.1;
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 AA; 13470 MW; FF0277F079783A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senotation update)
EPHRIN A3 (FRAGMENT).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                   118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 QFTMGPNVKINVLEDFEGENPQVPKLEKSISG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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125 KFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVP-TLPQ 183
                                                                                                                                                                                                        66 YNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQG-FKRWECNRPHAPHSPIKFSE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                      Gaps
                                                                                                  6 LLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPH 65
                                                                                                                                35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
Chen P.B., Rodger J., Dunlop S.A., Beazley L.D.;
"Ephrin homologs are expressed in the adult lizard visual system.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                 17;
Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 88;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=BRAIN;
Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF209777; AAF19444.1; -
InterPro: IPR010799; Ephrin.
Probom: PR00812; Ephrin.
Probom: PR0082533; Ephrin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 17, Last annotation update)
Query Match
32.6%; Score 424.5; DB 13;
Best Local Similarity 45.4%; Pred. No. 3.8e-36;
Matches 84; Conservative 28; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.2%; Score 406; DB 13;
Llarity 75.0%; Pred. No. 1.1e-34;
Conservative 7; Mismatches 9;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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Ctenophorus ornatus.
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Matches 72; Conserv
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
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                                                                   SEQUENCE FROM N.A.
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                            Cypriniformes; C
NCBI_TaxID=7955;
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Q9D7K8;
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Matches
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X MEDLINE-21085660; Pubbed=11217851;

X Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Hara A., Fukuhishi Y., Konno H., Adachi J., Fukuda S.,

A Alawawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

R Gadta K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

R Gasterland T., Gissi C., King B., Kochiwa H.;

R Lewis S., Mitsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blak J., Boffelli D., Bojuga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Lyons P., Marchioni L., Mashima J., Mazarelli J., Mombaerts P.,

Lyons P., Marchioni L., Mashima J., Mazarelli J., Mondone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Saluki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 SSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LIPLIRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPHYE 62
                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AK012195; BAB28092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2610529M21, FULL INSERT SEQUENCE.
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Last annotation update)
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46.9%; Pred. No. 3.3e-34;
tive 19; Mismatches 62;
               206 AA.
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                                         Created)
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               PRT;
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              PRELIMINARY;
                                   01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                              NCBI_TaxID=10090;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TOSSUE-TONGUE;

K MEDINE-21085660; DubMed-11217851;

K ATARAWA T., Shipata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alaawa T., Hara A., Nibata K., Konno H., Rasukawa T., Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

K Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

K Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

K Relischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

K Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Uyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYMVSRNGYRTCNA-SQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGE---- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 ALGNRHAVYWNSSNQHLRRECYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYV 87
                                                                                                                                                                                                                              Durbin L., Brennan C.H., Shiomi K., Cooke J.;
"Eph signalling is required for segmentation and differentiation of
Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 373; DB 13; Length 229; 40.0%; Pred. No. 1e-30; ive 25; Mismatches 59; Indels 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADULT MALE TOWNUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2310004J15, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                 Line Soultes: , ; submitted (Uni-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ006838; CAA07264.1; -. InterPro; IPR001799; Ephrin. InterPro; IPR003006; Ig_MHC. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN. ProDom: PE001293; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1. PROSITE; PS01299; EPHRIN; 1. PROSITE; PS01299; IG_MHC; UNKNOWN_1. SEQUENCE 229 AA; 26115 MM; 8684462F67AF6F5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 -- NP------QVPKLEKSI--SGTS 216
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hes 84; Conservative
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9

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[1]
SEQUENCE FROM N.A.
MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M., Wilson S.;
"The Pax protein Noi protein is required for commissural axon pathway formation in the rostral forebrain.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y12928, CAA73391.1;
ZFIN: ZDB-GENE-001128-1; efna5a.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
    35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
"Ephrin homologs are expressed in the adult lizard visual system.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF209776; AAF19443.1;
InterPro; IPR001799; Ephrin.
Probom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%; Score 268.5; DB 13; Length 93; llarity 49.5%; Pred. No. 2.4e-20; Conservative 18; Mismatches 22; Indels 9
                                                                                       108 WECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AA; 11323 MW; BD561F18D34C0F28 CRC64;
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 GYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || || : :|||||||||| : | | | ::||||||||::
GYLTCEHRMRGFKRWECNRPQSPDGPLRFSEKFQRFT 89
                                                                                                                                                                                                              93 AA.
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                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN-AS (FRAGMENT).
                                                                                                                                                                                                                                                                                                            EPHRIN A2 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                        Ctenophorus ornatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=95347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                 Ctenophorus.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                    09PTD1;
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042304
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynghaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ----MERYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFTPFILGKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Matsunaga T., Davis J.G., Greene M.I.;

Matsunaga T., Davis J.G., Greene M.I.;

Cellular sand subcellular compartmentalization of adult peripheral vestibular system by distinctive and overlapping expression of Eph receptors and ephrins.";

submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF131912: AAD13515.1;

InterPro; IPR001799; Ephrin.

Propom; PD00253; Ephrin: 1.

PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL: AK009144; BAB26102.1; -.
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                                                                                                                                                                                                                                                                                                                                                                          28.2%; Score 367; DB 11; Length 205; 38.3%; Pred. No. 3.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                             MGD; MGI:103236; Effal.
InterPro; IPR001799; Ephrin.
InterPro; IPR001080; WD40.
Pram; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODON; PD002533; Ephrin; 1.
PROSTIE; PS00078; MD_REPEATS_1; UNKNOWN_1.
SEQUENCE 205 AA; 23772 MW; E37E55767459AEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11838 MW; A497302F7FD7364B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 -FEGENPOVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 38.3 es 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                 Hayashizaki Y.;
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SEQUENCE
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Gaps

Last sequence update)
Last annotation update)

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70 AA.

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SEQUENCE FROM N.A.
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"A systematic search for the downstream target genes of the midbrain-
MHB reciprocal inductive signaling by ordered differential display
                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cyptiniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                revealed the expression of ephrin-A3 in the posterior tectum of zebrafish embryos.";
                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-201) to the EMBL/GenBank/DDBJ databases. EMBL; AB055674; BAB62805.1; -. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 70 AA; 7621 MW;
                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, D160 PROTEIN (FRAGMENT).
                                                                   PRELIMINARY;
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                                                                                090ZG7;
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                                     RESULT 12
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                                                                                                                                                                   46 REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGFGGGAEQYVLYMVSRNGYRTC-NASQG 104
                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLE) 17, Last sequence update)
01-JUN-2001 (TrEMBLE) 17, Last sequence update)
12 DAYS EMBRYO EMBRYONIC BODY BETWEEN DIAPHRAGM REGION AND NECK CDNA,
RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:9430025D14, FULL INSERT
SEQUENCE (FRAGMENT).
                                                                                                                                            Gaps
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                          DB 13; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 208; DB 11; Length 42;
Pred. No. 1.7e-14;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=EMBRYONIC BODY BETWEEN DIAPHRAGM REGION, AND NECK; MEDLINE-21085660; PubMed=11217851;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                          80 AA; 9674 MW; 712DDC6058214993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55DB95E5E0B1B0E2 CRC64;
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                                                                                          42 AA.
                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel, 17, Created)
01-JUN-2001 (TrEMBLrel, 17, 1act com
                                                                                                                                                                                                                                105 FKRWECNRPHAPHSPIKFSEKFORYS 130
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                               Mature 409:685-690(2001).
EMBL: AK020438; BAB32100.1; -.
                ProDom; PD002533; Ephrin; 1.
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97.6%;
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                                                                                                                                         Conservative
 Pfam; PF00812; Ephrin; 1
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                       Local Similarity
ses 44; Conserv
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Best Local Similarity
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                                           80
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NON_TER
SEQUENCE
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Matches
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91F2BE4E657E10FD CRC64;

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                                                                                                          CCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLA 225
                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-21290827: PubMed=11397014;
MEDLINE-21290827: PubMed=11397014;
MEDLINE-21290827: PubMed=11397014;
Thomas M.C., Cleary J.A., Bernan C., Fishman M.C., Roberts T.M.;
"Morphogenesis of prechordal plate and notochord requires intact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 331;
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     Length 70;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
13.7%; Score 178; DB 13;
54.1%; Pred. No. 4.4e-11;
ive 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 166.5; DB ilarity 26.8%; Pred. No. 5e-09; Conservative 28; Mismatches
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Dev. Blol. 234:470-482(2001).
EMB.; AF375227; AR64277.1; -
SEQUENCE 331 AA; 35638 MW;
                                                         Conservative
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                         Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 70; Conserv
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1 DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTLLAS

12 ILLIFLVDLLGITAT-----NMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSD 64

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Signal.
                      Q9PUJ4
RESULT 15
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MEDLINE-20099673; PubMed=10633856;
MEDLINE-20099673; PubMed=10633856;
MEDLINE-20099673; PubMed=10633856;
MEDLINE-20099673; PubMed=10633856;
MILKINGON D.G., Brandli A.W.;
"Comparative analysis of embryonic gene expression defines potential interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
Dev. Dyn. 216:361-373(1999)
EMBL; AJ236866; CAB65511.1;
InterPro; IPR001099; Ephrin.
                                                                                 157
          ---NGYRTCNASQGFKRWECNR 112
                                                      113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ----SRNGYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 KEEMSSCSILRTPNL----LLTCDR---PSQDLRFTIKFQEFSPNLWGHEFQSQRDYYI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ISTPTHNL------MGPNV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 IATSDGTMDGIETLQGGVCETKGMKVTLKV---GQSPNGATP-PRRPSSAGKDSGISPSV 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 IYWNSSNKRFEDTEGYVLYPQIGDRLDLLCPRSEPQ-----GPFSSSPYEYKLYLVGT 83
                                                                   173 SGEKPVPTLPQFTMGPNVK-----INVLEDFEGE--NPQVPKLEKSISGTSPKREH
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Stropus Laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniada; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 KINVLEDFEGENPQVPKLEKSISGTSPKR-----EHLPL----AVGIAFFLMTF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                    Query Match 12.6%; Score 164.5; DB 13; Length 327; Best Local Similarity 26.6%; Pred. No. 8e-09; Matches 63; Conservative 31; Mismatches 78; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. 4BB0FA39D4C22DCD CRC64;
                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                            327 AA.
      68 SSGVGPGAGPGGGA--EQYVLYMVSR------
                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                      213 LPASNIAVIAGAAGGSAFLLL 233
                                                                                                                                                      222 LP-----LAVGIAFFLM 233
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NCBL_TaxID=8355;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EPHRIN-B2 PRECURSOR.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 SNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPRSTDPTKRPEQEAGTNGKSSTTS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 NGYRTCNASQGFKRWECNRP----HAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIST 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 PTHNLH-------WKCLRMKVFVCCASTSHSGEKPVPT----LPQFTMGPNVKINV-- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 IYWNSSNPKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ-----YEYYKVYMVDK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQADSCAIRKD-----NTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNKDYYVIST
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Menzel P., Pasquale E.B.;

"Coding sequence of chicken ephrin-B2.";

Submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF180729; AAD53948.1;

InterPro; IPR001799; Ephrin.

Pfam; PF00812; Ephrin. 1.

Probom; P00012533; Ephrin, 1.

PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-B2.
4C28E8CB211B7783 CRC64;
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                                                        Created)
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Job time: 463 sec
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 333 E
333 AA; 36761 MW;
                                                     (TrEMBLrel. 13, TrEMBLrel. 13, (TrEMBLrel. 17,
PRELIMINARY;
                                                     01-MAY-2000
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 13, 2002, 10:45:35 ; Search time 24.34 Seconds (without alignments) 378.605 Million cell updates/sec Run on:

US-09-733-756-2 1301 1 MAAAPLLLELLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	D52747 homes omed	45 mus m	1 mus	homc	brach	_	٣	mus m	5 ratt		P52804 gallus gall		P20827 homo sapien	xenor		P52798 homo sapien		Q15768 homo sapien		P52799 homo sapien			073874 brachydanio	P52795 mus musculu	O13097 xenopus lae	P52796 rattus norv			Q12906 h interleuk	~	091il3 rattus norv	P11370 mus musculu	_
ID	EFA3 HUMAN	EFA3_MOUSE	EFA2_MOUSE	EFA2_HUMAN	EFA2_BRARE	EFA2_CHICK	EFA5_HUMAN	EFA5_MOUSE	EFA5_RAT	EFA4_MOUSE	EFA5_CHICK	EFA5_BRARE	EFA1_HUMAN	EFA1_XENLA	EFA1_MOUSE	EFA4_HUMAN	EFA1_RAT	EFB3_HUMAN	EFB3_MOUSE	EFB2_HUMAN	EFB2_MOUSE	EFB1_HUMAN	EFB2_BRARE	EFB1_MOUSE	_FB1_XENLA	EFB1_RAT	EFB1_CHICK	POLG_POL32	ILF3_HUMAN	CASP_MOUSE	ILF3_RAT	ENV2_MOUSE	KRUP_DROME
Length DB	1	187 1												216 1	205 1	201 1	205 1	340 1	340 1	333 1	336 1	346 1	332 1		327 1		334				•	432 1	466 1
% Query Match Le	100.0	74.	33	33	32	32	31	31	31	31.5	31.1	30.5	30.0	28.9	28.7	28.0	27.8	m	<b>m</b>	13.2	m,	4.1.	11.3	10.7	10.3	10.2	4.	0.	8.9	6.5	6.4	6.3	6.3
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P48432 mus musculu Q10462 caenorhabdi	Q9z1x4 mus musculu P51532 homo sapien	P38159 homo sapien P05877 human immun	P00722 escherichia	Q92826 nomo sapien P48431 homo sapien	P54231 ovis aries	P05315 solanum tub	P13677 drosophila
SOX2_MOUSE CAHX_CAEEL	ILF3_MOUSE SN24_HUMAN	ROG_HUMAN ENV_HV1MN	BGAL_ECOLI	HXBD_HUMAN SOX2_HUMAN	SOX2_SHEEP	CHIT_SOLTU	KPC2_DROME
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319	911	391 856	1023	317	320	328	700
6.3	6.2	6.1	0.0	9.0	0.9	6.0	0.9
82 82	81 81	79.5	78.5	78	78	78	78
34 35	36	36 36	0.7	47	43	44	45

# ALIGNMENTS

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EFA2_MOUSE
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                                                                                                                                                                                             IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                              KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                              Gaps
                                                                                                                                  1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                               Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1966).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                            181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                         EFA3_MOUSE STANDARD; PRT; 187 AA.
008545; 055217;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ephrin-a3 (EPH-related receptor tyrosine kinase ligand 3) (LERK-3)
(EHK1 Ligand) (EHK1-L) (Fragment).
EFNA3 OR EPLG3 OR LERK3 OR EPL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN REF. 2).
8EFD6AE8FE33FDDA CRC64;
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                                                                                    100.0%; Score 1301; DB 1; Length 238; 100.0%; Pred. No. 2.8e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-129;
MEDLINE-298126446; PubMed-9465306;
Cerretti D. P., Nelson N.;
"Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure.";
Genomics 47:131-135(1998).
                                                                                                             Indels
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SEQUENCE OF 17-78 FROM N.A.
MEDLINE=97060319; Pubmed=8903354;
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InterPro; IPR001799; Ephrin.
38
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26350 M
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  38
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100
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238 AA;
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                                                                                                             238;
             CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
   CARBOHYD
                                                                                     Query Match
                                                                                                  Best Local
Matches 23
                                                                                                                                                                                                                                                                                                                                                  EFA3_MOUSE
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53 GSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKV 112
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Efbrin-A2 precursor (EPH-reland receptor tyrosine kinase ligand 6)
(LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 FVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                 . .) (POTENTIAL). . .) (POTENTIAL). . .) (POTENTIAL). . .)
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                                                                                                                                                                                                                                                                                                              74.0%; Score 963; DB 1; Length 187; 91.3%; Pred. No. 1.3e-83; ive 3; Mismatches 6; Indels
                                                                                                 N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
Y-LINKED (GLCNAC. ..) (POT
Y -> I (IN REF. 2).
EQ -> DR (IN REF. 2).
RT -> QP (IN REF. 2).
Y -> W (IN REF. 2).
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Identification and cloning of ELF-1, a developmentally
ligand for the Mek4 and Sek receptor tyrosine kinases.";
Cell 79:157-168(1994).
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STRAIN-SWISS WEBSTER; TISSUE-Brain;
MEDLINE-95007776; PubMed=7522971;
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MEDLINE=95181289; PubMed=7876076;
                                                                                                                                                                                                                                                     21171 MW;
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                             GPI-anchor
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nes 178; Conserv
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                                                           Glycoprotein; GNOA_TER 21
NOA_TER 24
CARBOHYD 41
CARBOHYD 45
CONFLICT 19
CONFLICT 33
CONFLICT 46
CONFLICT 76
SEQUENCE 187
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P52801;
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25
29
213 AA;
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                                                                                                          SEQUENCE FROM N.A.
                                                                 Carrano A.V.;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SINDYLDIYCPHY-----GAPLPPAERMERYILYWVNGEGHASCDHRORGFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Gaps
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MEDLINE-98126446; PubMed=9465306;
MEDLINE-98126446; PubMed=9465306;
MEDLINE-98126446; PubMed=9465306;
MEDLINE-9812646; PubMed=9465306;
"Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3), mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
Conservation of infron/exon structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFA2_HUMAN STANDARD, PRT; · 213 AA.

15-08-1998 (Rel. 37, Created)
15-05-1999 (Rel. 37, Last sequence update)
15-07-2001 (Rel. 40, Last sequence update)
Ephrin-2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (HEX7-Ligand) (HEX7-L).
EFNAZ OR EPLG6 OR LERK6.
                                                                                                                                                                                                                                                                    EPHRIN-A2.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

F1997545F25B9ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 437; DB 1; Length 209; 50.5%; Pred. No. 4.9e-34; tive 25; Mismatches 47; Indels 3
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                          EMBL: U14752; AAAA88501; -
MGD; MGI:102707; Efna2.
InterPro; IPR001799; Ephrin.
PRIMTS; PR01347; EPHRIN.
PRODOM; PD002533; EPHRIN.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                               23586 MW;
                                                                                                                     EMBL; U14941; AAA53636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    96; Conservative
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209
38
170
184
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38
170 1
184 1
209 AA;
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173 LYEAPEPIFT 182
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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AC DERA2_H
AC DERA2_H
DT 15-DEC
DT 16-OCT
DE EPPLIN
DE CLERK-
GN EURAT
OC MAMMAN
OX NCBL C
NX NCBL C
RX MEDLI
RY CETE
RY CONSE
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Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;
"Cloning, chromosal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2.";
Biochem. Biophys. Res. Commun. 252:378-3821998).
-:- SUBGNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
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Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise Trankheim M., Amico-Keller G., Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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EPHRIN-A2.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
R -> A (IN REF. 3).
RA -> PP (IN REF. 3).
AA -> RR (IN REF. 3).
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                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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Matches 96; Conservative 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                    "Two Eph receptor tyrosine kinase ligands control axon growth and may be involved in the creation of the retinotectal map in the zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENT 124:655-664(1997).
-!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 YMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGFGGGAEQYVL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADED FASHION THROUGHOUT THE TECTUM.

SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                     01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
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40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 39, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine kinase ligand 6)
40-MAY-2000 (Rel. 30, Last annotation tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       B., Drescher U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (P. 9EE284FEB61D0C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 426; DB 1;
Pred. No. 4.9e-33;
4; Mismatches 38.
                                                                                                                                                                                                                                                                                                                                     R., Guthrie
      195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STPTHNLHWK-CLRMKVFVCCASTSHSGEKPVPTL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Neurogenesis; Gly
SIGNAL 1 16 POTENTIAL.
CHAIN 17 195 EPHRIN-A2.
                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=97195707; Pubmed=9043080;
Brennan C., Monschau B., Lindberg
Bonhoeffer F., Holder N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y09668; CAA70863.1; -. 2FIN; 2DR-GENE-990415-66; efna2. InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin, 1. PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin, 1. PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 AA; 22688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.7%;
52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
    STANDARD;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
EFA2_BRARE
P79727:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
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                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
10-MAY-2000 (Rel. 34, Last sequence update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
(LERK 6) (ELF-1).
Gallus aplus (Chicken).
Gallus gallus (Chicken).
Eukaaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Gallus archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 82:371-381(1995).
--- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND EPHA5 (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G., "Complementary gradients in expression and binding of ELF-1 and Mek4 in development of the topographic retinotectal projection map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
--- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
---- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAPLILLILLIVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
8FABIAESE41EED96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.4%; Score 421; DB 1; Length 200
47.5%; Pred. No. 1.5e-32;
ive 29; Mismatches 50; Indels
200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPY00199; Ephrin.
Pfam; PF00812; Ephrin.
PRINTS; PR01347; EPHRIN.
ProDom; PD00233; Ephrin. 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95360981; Pubmed=7634327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L40932; AAC42229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23049
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nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
161
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
36
161
175
200 AA;
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173 T 173

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K., "LERK-7: a ligand of the Eph-related kinases is developmentally regulated in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95267434; PubMed=7748564;
Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
Tsai S.P., Goddard A., Henzel W.J., Hefti F.;
"Cloning of AL-1, a ligand for an Eph-related tyrosine kinase
receptor involved in axon bundle formation.";
                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPHRIN-A5.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20069483; PubMed=10601038;
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=97392664; PubMed=9245480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U26403; AAB60377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine 9:540-549(1997).
                                                                                                                  (LERK-7) (AL-1).
EFNAS OR EPLG7 OR LERK7.
                             STANDARD;
                                                                                                                                                                                                                                                                                                             Neuron 14:973-981(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
228
37
                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICRODOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 601535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism
                            EFA5_HUMAN P52803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
RESULT 7
EFA5_HUMAN
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCES COMPARTMENTIAL DESIGNATION A CAVECLAR FACALICATION.

INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVECLAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE BY SIMILARITY).

-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1 (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVECLAE-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCTS BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                               67 NSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                         126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                   LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI------PSR-----LLAI 217
                                                                                                                                                                        99
                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
-!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G., "Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                               EDS------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                      8 LLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                  47;
                                                                                                Length 228;
                                                                                                                                    Indels
  N -> K (IN DBSNP:469062).
                                      6893B1CCACFF3F57 CRC64;
                                                                                Score 415.5; DB 1;
Pred. No. 5.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          008543; 008544;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                      /FTId=VAR_012035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE-97060319; PubMed-8903354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LERK-7) (AL-1).
EFNA5 OR EPLG7 OR LERK7 OR EPL7.
                                                                                                                                  37;
                                      MW.
                                                                                              31.9%;
                                      26297
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Wonse)
                                      228 AA;
                                                                                            Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 AFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 LLFLLAML 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFA5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                      SEQUENCE
VARIANT
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EFA5_MOUSE
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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SEQUENCE
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                                     Pfam; PF00011: Ephini: 1.

PRINTS; PR01347; EPHRIN: 1.

ProDom; PD002533; Ephrin; 1.

PROSITE; PS01299; EPHRIN: 1.

Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal; Alternative splicing.

SIGNAL
                                                                                                                                                                                                                                                                                                                         126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                      67 NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                            66 EDS------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117
                                                                                                                                                                                                                                                                                                                                                                   181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                    8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                                 MEDLINE-95267434; PubMed-7748564; Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.O., Wong S.C., Tsai S.P., Goddard A., Henzel W.J., Hefti F., Beck K.D., Caras I.W.; "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved in axon bundle formation."; Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li Y.Y., McTiernan C.F., Feldman A.M.;
"referry, rat ligand for Eph-related receptor tyrosine kinase.";
Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases.
-i- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                 EPHRIN-A5.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
85439F5337420022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                  47;
                                                                                                                                                                                           DB 1; Length 228;
                                                                                                                                                                                          ; Score 414.5; DB 1; Length; Pred. No. 7.1e-32; 36; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                           MM;
EMBL; U90664; AAB50239.1; -.
                      MGD; MGI:107444; Efna5.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                         31.9%;
                                                                                                                                                          26339
                                                                                                                                                                                                               98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LERK-7) (AL-1).
EFNA5 OR EPLG7 OR LERK7.
                                                                                                            20
228
37
189
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STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AN STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                          228 AA;
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              229 AFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                   218 LLFLLAML 225
                                                                                                                        21
37
163
                                                                                                                                            VARSPLIC
SEQUENCE
                                                                                                                                   CARBOHYD
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P97605:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).

-!- SUBURIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1 (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 EDS------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI-----PSR-----LLAI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFA4_MOUSE STANDARD; PRT; 206 AA.
008542; 055218;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
855985532D580022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.9%; Score 414.5; DB 1
39.5%; Pred. No. 7.1e-32;
ive 36; Mismatches 67
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EFNA4 OR EPLG4 OR LERK4 OR EPL4.
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InterPro; IPR001799; Ephrin.
Pfam; PF00012; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 N
26358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.99
Best Local Similarity 39.55
Matches 98; Conservative
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228 AA;
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SIGNAL
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      OC GREEN
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                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 S------PGPPEGPETFALXMVDWSGYEACTAEGANAFQRWNCSMPFAPFSPVRFSEK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN. 67
          Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.; "Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis."; Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
20-MAY-2010 (Rel. 39, Last annotation update)
(LERK-7) (RAGS protein).
EFNAS OR RAGS.
                                                                                                       Cerretti D.P., Nelson N.; "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3), mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6): conservation of infron/exon structure.";
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.5%; Score 410; DB 1; Length 206; 47.4%; Pred. No. 1.7e-31; tive 18; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43501971DD1C6EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL ATTACHMENT SITE
                                                                                                                                                                               similarity).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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EMBL, U92890; AAC39962.1; -.
EMBL, U92889; AAC39962.1; JOINED.
MEDLINE=97060319; PubMed=8903354;
                                                                                              MEDLINE=98126446; PubMed=9465306;
                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1347; EEHRIN.
PRODENTE; PRO1293; EPHRIN; 1.
PROSITE; PSO1299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA; 22861 MW;
                                                                                                                                                                                                                                                                                                                                           MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                         Genomics 47:131-135(1998)
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98
43
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                  STRAIN=129;
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P52804;
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Best Local Si
Matches 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00012; Ephrin: 1.
PRIMES: PR01347; EPHRIN.
PROSITE: PS01293; EPHRIN: 1.
PROSITE: PS01299; EPHRIN: 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                           MEDLINE-95360980; PubMed-7634326; Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda M., Bonhoeffer F.; "In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDatectal protein related to ligands for Eph receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 82:359-370(1995).
-1- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL GANGLION CELL AXONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
(LERK-7) (AL-1) (ZFEPHL4).
EFNA5 OR EFNA5 OR ALI OR EPLG7 OR LERK7.
ENA5 OR EFNA5 OR ALI OR EPLG7 (SECHANIO).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQQGDYHIDVCINDYLDVFCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .31.1%; Score 404.5; DB 1; Length 228; 49.1%; Pred. No. 6.2e-31; tive 29; Mismatches 42; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (P
56D8E4FBDECF18AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
EPHRIN-A5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 37 37
228 AA; 26206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X90377; CAA62027.1; -.
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                                                                                                                                                                                                                        TISSUE-Posterior tectum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
228
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFA5_BRARE
P79728;
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factor, alpha-induced protein 4).
EFNA1 OR EPGL1 OR LERK1 OR TNFAIP4.
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                            -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
                                                                                                     may
                                                                                                                                                                             67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDS-----VPEERTERYVLYMONYDGYSTCDHTAKGFKRWECNRPHSPNGPLKFSEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LLLLVPVPL-LPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY:66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (Immediate early response protein B61) (Tumor necrosis
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                         Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U., Bonhoeffer F., Holder N.;
"Two Eph receptor tyrosine kinase ligands control axon growth and be involved in the creation of the retinotectal map in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL) 74B3406C05418E6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.5%; Score 397; DB 1; Length 228; 47.8%; Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-A5.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y09669; CAA70864.1; -. 2FIN; ZDB-GRE-9805286-186; efna5b. InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin, I. ProDom; PD000533; Ephrin; I. ProDom; PD000533; Ephrin; I. PROSITE; PS01299; EPHRIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                     TISSUE=Embryo;
MEDLINE=97195707; PubMed=9043080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 37 N
228 AA; 26595 MW;
                                                                                                                                  Development 124:655-664(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
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Best Local Similarity
                                          FROM N.A.
                     NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFA1_HUMAN P20827;
                                                                                                                      zebrafish.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Ligands for the receptor tyrosine kinases hek and elk: isolation of CDNAs encoding a family of proteins."; oncogene 10:299.306(1995).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4, EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.-!- INDUCTION: BY TNF-ALPHA AND INTERLEUKIN-1 BETA.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95140419; PubMed-7838529;
Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
Cerretti D.P., Beckmann M.P.;
                                                                                                                                                                                                                                                            of endothelium is induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA---
                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 26 N-LINKED (GLCNAC. . .) (POTENTIAL). 205 AA; 23771 MW; 4FEFC6BF4C1251A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 205;
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 390; DB 1;
41.8%; Pred. No. 1.3e-29;
ive 21; Mismatches 76
                                                                                                                                                                                          MEDLINE=91042512; PubMed=2233719;
Holzman L.B., Marks R.M., Dixit V.M.;
"A novel immediate-early response gene of en
cytokines and encodes a secreted protein.";
Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PEVRVLHSIGHSAAPRL--FPLA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A36377; A363777.

MIM; 191164; -
InterPro; IPR01799; Ephrin.
Pfam; PF001312; Ephrin. 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
Glycoprotein; GF1-anchor; Signa SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M57730; AAA58388.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. ) (POTENTIAL).
TPPPVNVHTPRSHIOSDEPEVPLPGYMKSVACNSAAPGTPC
TLYGLLLAALLLRL -> SE (IN ISOFORM A').
1B3A508E0A7B872E CRC64;
                                                                                                                                                                                                                                                                                    Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A.;
"Embryonic expression of eph signalling factors in Xenopus.";
Mech. Dev. 57:133-144(1996).

-1- SUBBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1 (BY

    -! SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQV-. 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 ISKPIHYHGETCMRLRVHV-----SGRTTPPPVNVHTPRSHI-------QSDEPEVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AQGERHIVFWNSSNYRFWQEDYTVQVQLNDYLDIVCPYYEEGSVA-----GHTVERYT 78
                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ebhrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (XELF)
EFNAI OR EPGLI OR ELF
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYV 87
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.9%; Score 375.5; DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPI-anchor; Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.1e-28, 25; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-! - SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
   216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-A1
   PRT;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=97000306; PubMed=8843391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AA; 24755 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U31204; AAA74485.1; -. EMBL; U31205; AAA74486.1; -. INTECPPO; IPRO01799; Ephrin. Prants; PRO1347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.18;
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STANDARD;
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LPGVMKSVAGNS 195
                                                                                                                                                                                                    Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
EFA1_XENLA
P52794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RESULT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97060319; PubMed=8903354;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Eph-related receptor tyrosine kinases during mouse embryogenesis.";
EPh-SIBGINIST TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
FFAI_MOUSE STANDARD, PRT; 205 AA.
PS2793; P97331;
01-0CT-1996 [Rel. 34, Created)
01-0CT-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Bephin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (Immediate early response protein B61).
Mus musculus (Mouse).
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C;
Morris J.C., Clarletta A., Morris G.E., Giannotti J., Caruso A., Hammett D.J., Finnerty H., Turner K., Wood C.R.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahashi H., Ikeda T.;
"Molecular cloning and expression of rat and mouse B61 gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REF. REF. REF. REF. REF. REF. REF.
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N-LINKED (
H -> Y (IN
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95405853; PubMed-7675446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             implications on organogenesis.";
Oncogene 11:879-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00812; Ephin; PRINTS; PR01347; EPHRIN.
Probom; PB002533; Ephrin; 1.
RNSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D38146; BAA07344.1; -. EMBL; U26188; AAA67563.1; -. EMBL; U90662; AAB5037.1; -. MGD; MGI103236; Efnal. InterPro; IPR001799; Ephrin.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ICR
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CARBOHYD
     HERE THE THE TELEFTER TO DESCRIPTION OF THE TRANSPORT OF
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9
                                                                                                                  138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                    Gaps
                                                                           26;
                                     Ouery Match 28.7%; Score 374; DB 1; Length 205; Best Local Similarity 38.7%; Pred. No. 4e-28; Matches 86; Conservative 23; Mismatches 87; Indels 2
 204 204 S -> T (IN REF. 1).
205 AA; 23802 MW; 5ABF3A6E2091E868 CRC64;
                                                                                                                                                                                               198 -FEGENPOVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                            165 RLGADDPEVQVLHSIGYSAAPRL--FPLVWAVLLLPLLLLQS 204
 CONFLICT
FT
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Db
                                                                                                                 Qy
Db
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Db
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Search completed: July 13, 2002, 10:53:18 Job time: 463 sec

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July 13, 2002, 09:55:25 ; Search time 42.58 Seconds (without alignments) 537.089 Million cell updates/sec
                                                                                                                                                                           US-09-733-756-2
1301
1 MAAAPLLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             283138 seqs, 96089334 residues
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                              Title:
Perfect score:
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                                                                                                       Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		TERRYS - Property	c	ephrin-A2 - himan	LERK-7 precursor -	repulsive axon qui	B61 protein precur	LERK-4 - human	ε		elk ligand - human	al	Ω	+	eti	genome polyprotein	beta-D-galactosida	beta-D-galactosida	hypothetical prote				O)	transcription fact					hypothetical profe	4
SUMMARIES		49	4	22	20	84	7.7	20	<b>4</b> 3	99	93	45	30	90	55	27	78	56	36	12	73	14	33		14	7.2	53	00	32	02
S		I38849	A54984	JE0322	158170	A57084	A36377	138850	184743	1497	8469	T32645	1487	I58406	T40265	GNNY 27	E90678	A85529	T21336	T28712	T19173	S67744	A2548	TWFF	T19914	T16772	B84463	A48830	A75132	150620
	DB	. 7	7	7	7	~	7	7	7	7	7	7	~	~	~	7	7	?	7	7	7	7	7	-	~	7	~	~	7	7
	Query Match Length	238	209	213	228	228	205	201	333	336	346	462	345	345	356	2206	1024	1024	817	709	1027	488	432	466	237	334	376	728	1144	1173
of	Query	100.0	33.6	33.4	31.9	31.1	30.0	28.0	13.2	13.2	11.4	11.0	10.7	10.2	7.7	7.0		8.9	6.7				6.3		6.3		6.3	٠		6.3
	Score	1301	437	434	415.5	404.5	9	364.5	171.5	171.5	148.5	143.5	139.5	132.5	100	91	88.5	88.5	87	85.5	84	83.5	82.5	82.5	82	82	82	82	82	81.5
	Result No.	H	7	3	4	5	9	7	ω.	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	protein BRG1 - hum	SNF2beta protein -	alkaline phosphata	reversed polarity	env polyprotein pr	phytocyanin At2944	probable protein w	beta-galactosidase	hypothetical prote	transcription fact	chitinase (EC 3.2.	protein kinase C (	genome polyprotein	genome polyprotein	thermopsin precurs
T19109	839059	545252	B72410	A54282	VCLJMN	T01605	B84789	GBEC	T13389	138238	S05426	A32392	GNNY 4 P	S03822	H90370
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		_	•	~	_	~	•					_			_
457	1613	164	43,	61;	85	202	498	1024	1291	321	328	700	2206	2206	57(
6.2 457	6.2 1613	6.2 164	6.1 43	6.1 613	6.1 859	6.0 203	6.0 498	6.0 1024	6.0 1291	6.0 321	6.0 328	0.9	6.0 2206	6.0 2206	6.0 570
81 6.2 457	81 6.2 1613	6.2	6.1	79 6.1 613	6.1	0.9	0.9	6.0	6.0	6.0	0.9	6.0	78 6.0 2206	78 6.0 2206	77.5 6.0 570

## ALIGNMENTS

RESULT

283138

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118RK 3 - human C.Species: Homo sapiens (man) A.Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs A.Recession: 13849 A.Accession: 13849 A.
Libra 1  Libra 2  Libra 3  Libra 3  Libra 4  Libra 5  Libra 4  Libra 5  Libra 5  Libra 5  C; Detces: Homo sapiens (man)  C; Detces: Homo sapiens (man)  C; Detces: 138849  R; Rozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepo oncogene 10, 299-306, 1995  R; Rozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepo norogene 10, 299-306, 1995  A; Pittle: Ligands for the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hek and elk: isolication to the receptor tyrosine kinases hekes  A; Reference number: 138849  A; Reference number: 1
Libbato Libbat
Libera - human C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #tex C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #tex C;Accession: 138849 R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; Vanden Oncogene 10, 299-306, 1995 A;Title: Ligands for the receptor tyrosine kinases hek A;Reference number: 138849; MUD:95140419 A;Reference number: 138849; MUD:95140419 A;Residues: Preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-238 <res> C;Genetics: references: EMBL:U14187; NID:9642832; PIDN:AAC5 C;Genetics: references: GDB:438336; OMIM:601381 A;Map position: 1421-1422 C;Genetics: references: GDB:438336; OMIM:601381 A;Map position: 1421-1422 C;Superfamily: axon guidance signal protein A;Map Position: 1421-1422 A;Map Pos</res>
Libers 19849 Libers 29-human C;Spate: 29-May-1998 #sequence_revision 29-May-19 C;Date: 29-May-1998 #sequence_revision 29-May-19 C;Accession: 138449 R;Kaclosky, C.J; Maraskovsky, E.; McGrew, J.T.; Oncogene 10, 299-306, 1995 A;Title: Ligands for the receptor tyrosine klnas. A;Reterence number: 138849; MUD:95140419 A;Accession: 138849 A;Cross-references: EMBL:U14187; NID:9642832; PII A;Map position: 1q21-1q22 C;Genetics: A;Genetics: A;Geneti
LERK-3 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29 R;Accession: 138849 R;Accession: 138849 A;Accession: 138849 A;Status: preliminary; translated from GB, A;Accession: 138849 A;Accession: 138849 A;Accession: 138849 A;Accession: 138849 A;Accession: 138849 A;Molecule type: mRNA A;Residues: 1-238 <res> A;Cross-references: EMBL:U14187; NID:g6428 A;Cross-references: EMBL:U14187; NID:g6428 A;Cross-references: GBB:438336; OMIN:60138 A;Conetics: A;Gene: GDB:EPLG3 A;Map position: 1q21-q22 C;Superfamily: axon quidance signal protes C;Superfamily: axon quidance signal protes C;Superfamily: axon quidance signal protes Matches 238; Conservative 0; Misma QY I                                      </res>
LERK: 3 - human C;Species: Home sapiens (man) C;Date: 29-May-1998 #sequence_revis C;Accession: 13849 R;Xc2losky, C.J.; Marcakovsky, E.; Oncogene 10, 299-306, 1995 A;Title: Ligands for the receptor it and the complex of a scale of a scale of the complex of a scale of the complex of a scale of a scale of the complex of a scale of a scal
LERKY 3 - human C, Species: Homo sapiens (mai C, Species: Homo sapiens (mai C, Date: 29-May-1998 #sequen C, Accession: 138849 R, Kozlosky, C. J.; Maraskovs  Oncogene 10, 299-306, 1995 A, Title: Ligands for the red A, Reference number: 138849; A, Accession: 138849 A, Status: preliminary; tran A, Molecule type: mRNA A, Residues: 1-238 < RES A, Cross - references: EMBL:U1- C, Genetics: GDB:EDLG3 A, Gross - references: GDB:438 A, Cross - references: GDB:438 A, Gross - references: GDB:438 A, Gross - references: GDB:438 A, Gross - references: GDB:438 A, Map Position: 1q21-1q22 C, Superfamily: axon guidance C, Superfamily: Axon guidanc
LERKA 3 - human C, Species: Home sapie C; Date: 29-Nay-1998 4 C; Accession: 138849 R; Kozlosky, C.J; May Oncogene 10, 299-306, A; Title: Ligands for A; Reference number: 1 A; Accession: 138849 A; Status: preliminary A; Molecule type: mRNP A; Residues: 1-238 CRR A; Cross-references: E C; Genetics:
138849 LERK-3 - humar C;Species: Hon C;Date: 29-May C;Accession: 10 R;KOzlosky, C. Oncogene 10, 2 A;Title: Ligan A;Reforence A;Reforence A;Residue: pred A;Residue: pred A;Residue: pred A;Residue: 1/A;Residue: 1/A;
138849 LERK-13 - C, Species C, Date: C, Access R, Kozlos R, Refere A, Refere A, Refere A, Refere A, Gene: A, Gene: A, Gene: A, Gene: A, Map po C, Superf, Db
COUNTY AND

A54984
BLF-1 protein precursor - mouse
BLF-1 protein precursor - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (sequence\_revision 11-Nov-1994 #text\_change 29-Sep-1999
C.Accession: A54984, A558873
B.Cheng, H.J.; Flanagan, J.G.

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C; Accession: 158170; G01812
R; Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.
R; Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.
A; Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involv
A; Reference number: 158170; MUID:95267434
A; Recession: 158170
A; Residues: 1-228 <RES>
A; Cross-references: GB:S77167; NID:9914184; PID:9914185
A; Cross-references: GB:S77167; NID:9914184; PID:9914185
A; Reference number: G08477
A; Reference number: G08477
A; Reference number: G08477
A; Molecule type: MRNA
A; Residues: 1-228 <RCS>
A; Cross-references: EMBL:U26403; NID:91019430; PIDN:AAB60377.1; PID:91019431
A; Residues: 1-228 <RCS>
A; Cross-references: EMBL:U26403; NID:91019430; PIDN:AAB60377.1; PID:91019431
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C; Species: Gallus gallus (chicken)
C; Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C; Accession: A57084
R; Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F
A; Drescher, Distro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal pr
A; Reference number: A57084; MUID:95360980
            117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 NSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI------PSR-----LLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 415.5; DB 2
llarity 39.5%; Pred. No. 1.9e-31;
Conservative 37; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Gene: GDB:EPLG7; AF1; LERK7
A)Cross-references: GDB:568757; OMIM:601535
A)Map position: 13q33-13q33
C; Superfamily: axon guidance signal protein
                                                             SHSGEKPVPT 180
                                                                                                            LYEAPEPIFT 186
                                                                                                                                                                                                                                   LERK-7 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                             N;Alternate names: AL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 LLFLLAML 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 98
                                                           171
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                                                                                                                                           A;Cross-references: GB:U14941; NID:9558836; PIDN:AAA53636.1; PID:9558837
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: CDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase A;Reference number: A55873; MUID:95181289
A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for A;Reference number: A54984; MUID:95007776
A;Accession: A54984
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A;Residues: 1-213 <AAS>
A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ephrin-A2 - human
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cista Gibber His Pedeutuur, F.; Grosgeorge, J.; Logtenberg, T.
Biochem Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of the gene encod
A;Reference number: JB0322; MUID:99045414
A;Recession: JB0322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQXVLYMVSRNGYRTCNASQ-GFKRWECNR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                            PIDN:AAA68520.1; PID:9681887
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Best Local Similarity 50.5%; Pred. No. 3.2e-33;
Matches 96; Conservative 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 33.6%; Score 437; DB 2;
1 Similarity 50.5%; Pred. No. 1.6e-33;
96; Conservative 25; Mismatches 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U14752; NID:g681886;
C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 LYEAPEPIFT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                               A; Molecule type: mRNA
A; Residues: 1-209 <CHE>
                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-209 <SHA>
                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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Gaps 99 CDNAS

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C:Species: Homo saplens (man)
C:Species: Homo saplens (man)
C:Date: 24-May-1996 #text_change 05-Nov-1999
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C:Accession: I8473
R:Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matt Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A:Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine A:Reference number: 149766; MUID:95199264
A:Actaus: preliminary; translated from GB/EMBL/DDBJ
A:Actaus: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Molecule type: mRNA
A:References: GB:L38734; NID:9769675; PIDN:AAC41752.1; PID:9769676
C:Genetics:
A:Cross-references: GB:L38338; OMIM:600527
A:Cross-references: GBB:A38339; OMIM:600527
Oncogene 10, 299-306, 1995
A.Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of A.Reference number: 138849; MUID:95140419
A.Acession: 138850
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-201 < RES>
A.Cross references: EMBL:U14188; NID:9642834; PIDN:AAC50079.1; PID:9642835
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS----PFGHVQFSEK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGSLEGLDNQEGGVCQTRAMKIL-MKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQADRCTIKKE-----NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIIST 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LILLLUVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 IYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ-----YEYYKVYWVDK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 FORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.0%; Score 364.5; DB 2 44.5%; Pred. No. 9.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
184743
hepatoma transmembrane kinase ligand - human
                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
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Matches 77; Conservative
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C:Accession: A36377
R:HOlzman, L.B.; Marks, R.M.; Dixit, V.M.
Mol. Cell. Biol. 10, 5830-5838, 1990
A:Title: A novel immediate-early response gene of endothelium is induced by cytokines A:Title: A novel immediate-early response gene of endothelium is induced by cytokines A:Title: A novel immediate and A:Title: A novel immediate and A:Title: A novel immediate and A:Molecule type: Mulary
A:Molecule t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 EDS------VPEDKTERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPNGPLKFSEK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ----MEOYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFORFTPFTLGKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS------PQAHVNPQEKRLAADD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                A)Cross-references: GB:X90377; NID:91061113; PIDN:CAA62027.1; PID:9984118 C;Superfamily: axon guidance signal protein
C;Keywords: 91ycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; not compared with conceptual translation Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 FQLFTPFSLGFEFRPGFEYFYISSAIPDNGRRSCLKLKVFV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                        31.1%; Score 404.5; DB 2;
49.1%; Pred. No. 2e-30;
live 29; Mismatches 42;
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4.1e-29;
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                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 49.1%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B61 protein precursor - human
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Best Local Similarity
Matches 87; Conserv
                                                                                                                       1-228 <DRE>
                     A; Accession: A57084
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                                                    A;Status: pre
A;Molecule ty
A;Residues: 1
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Species: Mus musculus (house mouse)
C;Species: Mus musculus (house musculus)
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Doll Bev. Biol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryons A;Reference number: 148780
A;Reference number: 148780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-345 <RESS
A;Coss references: EMBL:248781; NID:9747858; PIDN:CAA88695.1; PID:9747859
A;Cross references: EMBL:248781; NID:9747858; PIDN:CAA88695.1; PID:9747859
Genomics 24, 127-132, 1994
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A:Accession: A55507
A:Actession: A55507
A:Status: preliminary
                                                                                                                                                                                                              Cipecies: Caenorhabditis elegans
Cipecies: Caenorhabditis elegans
Cipate: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
Cipate: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
Cipate: 30-oct-1999 #sequence_revision 29-oct-1999
Ricatung, S. 160ela
Ricatung, D.; Harper, M.
Submitted to the EMBL Data Library, December 1997
Ricatus: The sequence of C. elegans cosmid F56All.
A:Reference number: 221204
A:Reference number: 221204
A:Reference number: 221204
A:Residue: 1-462 cgar>
A:Residues: 1-462 cgar>
A:Residues: 1-462 cgar>
A:Cross-references: EMBL:AF038619; PIDN:AAB92075.1; GSPDB:GN00022; CESP:F56All.3
A:Experimental source: strain Bristol N2; clone F56All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 FSEKFQRYSAFSLGYEFHAGHEYYYISTPT-----HNLHWKC-----LRMKVFVCCA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSHSGEKPVPTLPQFTMGPNVKINVL---EDFEGENPQVPKLEKSISG-TSPK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                hypothetical protein F56All.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 143.5; DB 2; 23.1%; Pred. No. 1.5e-05; Live 30; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3
                                189 NVKINVLEDFEGENPQVPKLEKSISGTS
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Best Local Similarity
Matches 54; Conserv
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                                                  QΩ
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                                   heptoma transmembrane kinase ligand - mouse

C;Species: Wus musculus (house mouse)

C;Species: Wus musculus (house mouse)

C;Accession: 149766

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews

Proc. Natl. Acad. Sci. US.A. 92, 1866-1870, 1995

A.Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin

A;Reference number: 149766

A;Reference number: 149766

A;Residues preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-336 <RES>

A;Cross-references: GB:L38847; NID:9769677; PIDN:AAC42052.1; PID:976978
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A)Title: Molecular characterization of a family of ligands for eph-related tyrosine kina
A, Reference number: 846993; MUD:94349923
A, Accession: 846993
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-346 < BEC>
A, Residues: 1-346 < BEC>
A, Cross-references: GB:U09304; NID:9538366; PIDN:AAA53093.1; PID:9538367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 NLH------WKCLRMKVFVCC---ASTSHSGEKPVPT-LPQFTMGPNVKINVLEDFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 MVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 TPTHNLH------WKCLRMKVFVCCA------STSHSGEKPVPTLPQFTMGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 IYWNSSNSKFLPGQGLVLXPQIGDKLDIICPKVDSKTVGQ-----YEYYKVYMVDK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 NRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEA------GRPYEYKLY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 171.5; DB 2; ilarity 28.3%; Pred. No. 2.4e-08; Conservative 27; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 GENPQVPKLEKSI--SGTSPKREHLPLAVGIAFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 KPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFI 242
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Pred. No. 3.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
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A Molecule Type: genomic RNA
A Residues: 1-2206 4-4405
A Cross-references: GB:X04468; NID:g61112; PIDN:CAA28155.1; PID:g61113
C; Superfamily: poliovirus genome polyprotein
F; 1-69/Product: coat protein; perome-linked protein; nucleotidyltransferas
F; 70-340/Product: coat protein VP2 #status predicted <VP2>
F; 70-340/Product: coat protein VP3 #status predicted <VP3>
F; 579-878/Product: coat protein VP1 #status predicted <VP3>
F; 879-1027/Product: coat protein P2-3b #status predicted <P3B>
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N;Contains: coat protein VP1; coat protein VP2; coat protein VP4;
N;Contains: coat protein VP1; coat protein VP2;
C;Coates: human polymerase (EC 2.7.7.48)
C;Species: human poliovirus 3
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Ju1-1999
C;Accession: A27245
J; Gen. Virol. 67, 2093-2102, 1986
A;Rithe: The nucleotide sequence of a type 3 poliovirus isolated during a recent out A;Reference number: A27245
M;Reference number: A27245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPDB:GN00067; SPDB:SPBC337.12
                                                                                                                                                                                                                                                                                                                                                       hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces pombe) (Schizosaccharomyces pombe cipates Schizosaccharomyces pombe cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 (CiAccession: T40265 Filther, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. Rajandream, M.A.; Barrell, B.G.; Rieger, M. Sabmitted to the EMBL Data Library, October 1998 A;Reference number: 221868 A;Reference number: 221868 A;Reference number: 221868 A;Retus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-356 <LXN> A;Residues: 1-356 <LXN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NGYRTCN------ ASQGFKRWECNRPHAPHSPIKFSE-----K 125
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                                                                 159 KIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQAPG--RGSQGDSDGKHETVNQQEK
                            ---STSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 TICPKFLNGRCNKAEDCNLSHELDPRRIPACRYFLLGKCNNPNCRYVHIHYSENAPICFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSR-
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19.0%; Pred. No. 0
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Matches 42; Conserv
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                         KVFVCCA-
                                                                                                                                                           211 SISG 214
                                                                                                                                                                                                                         SGPG 220
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R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.

J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyr

A;Reference number: A55062; MUID:95014510

A;Accession: A55062

A;Status: preliminary: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, Tr, 91-345 <SHA>

A;Cross-references: GB:UI2983; NID:9575928; PIDN:AAA53231.1; PID:9575929

G;Genetics:

A;Gene: EPLC2
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C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C; Accession : 158406
N; Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Holling, A; Title: LERR-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser A; Reference number: 158406; MUID:95022634
A; Accession: 158406
A; Accession: 158406
A; Accession: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-345 < RES>
A; Molecule type: mRNA
A; Cross references: EMBL:U07560; NID:9563118; PIDN:AAA53092.1; PID:9563119
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 CPRAEA-----GRPYEYYKLYLVRPEQAAACSTVLDPNVLVTCN------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 APLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 NRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLH--------WKCLRM 161
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; Pred. No. 0.00011;
27; Mismatches 88; Indels 71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 RYSAFSLGYE-------FHAGHEYYYISTPTHNLHWKCLRMKVFVCCAST 170
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                   26 GGALGNRHAV--YWNSSNQHLRREGYTVQVN----VNDYLDIYCPHYNSSGVGPGAGPG 78
F;1028-1124/Product: core protein P2-5b #status predicted <P5B>
F;1125-1453/Product: core protein P2-X #status predicted <P2X>
F;11454-1540/Product: protein P3-1b #status predicted <P1B>
F;1541-1562/Product: genome-linked protein VPG #status predicted <VPG>
F;1541-1562/Product: proteinase #status predicted <PTS>
F;1563-1745/Product: proteinase #status predicted <PTS>
F;1746-2206/Product: RNA-directed RNA polymerase #status predicted <RNS>
F;1746-2206/Product: RNA-directed TNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                           Query Match 7.0%; Score 91; DB 1; Length 2206; Best Local Similarity 20.5%; Pred. No. 8.1; Matches 52; Conservative 29; Mismatches 109; Indels
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246 DYLLGCGVLIGNAF 259
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Search completed: July 13, 2002, 10:46:37 Job time: 3072 sec

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; MOLECULE TYPE: protein US-08-240-124-2
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-057-121-2

US-09-258-73-121-2

US-08-255-001-2

US-08-38-734-2

US-08-308-814-2

PCT-US95-11869-2

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-492-10

US-09-173-13-10

US-09-173-13-10

US-09-173-13-10

US-09-173-13-10

US-09-173-13-10

US-09-048-129-2

US-09-09-3244-2
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                                                                                                                                                                                                                                                                                                                                                                                                    231628 seqs, 24425594 residues
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Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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1301
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Match I
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Perfect score:
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Maximum DB
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Sequence 8, Appli	US-08-920-440B-8	0	104	25.7	334	45
ω,	US-09-609-324A-8	-	104	25.7	334	44
Sequence 4, Appli	US-09-358-734-4	4	201	28.0	364.5	43
Sequence 4, Appli	US-09-057-121-4	7	201	28.0	364.5	42
Sequence 4, Appli	US-08-453-943-4	-	201	28.0	364.5	41
Sequence 4, Appli	US-08-240-124-4	<b>—</b>	201	28.0	364.5	40
Sequence 5, Appli	PCT-US95-11869-5	S	179	28.0	364.5	39
Sequence 5, Appli	US-08-455-001-5	<del>, -</del>	179	28.0	364.5	38
Sequence 12, Appl	US-08-959-524-12	m	205	30.0	390	37
Sequence 1, Appli	US-08-959-524-1	٣	205	30.0	390	36
Sequence 12, Appl	US-08-445-065-12	N	202	30.0	390	35
Sequence 1, Appli	US-08-445-065-1	~	202	30.0	390	34
Sequence 4, Appli	US-08-299-567-4	~	205	30.0	390	33
Sequence 1, Appli	US-08-452-779-1	H	205	30.0	390	32
Sequence 2, Appli	US-08-441-216-2	П	205	30.0	390	31
Sequence 1, Appli	US-08-448-736-1	-	205	30.0	390	30
Sequence 2, Appli	US-08-321-162-2	-	202	30.0	390	29
Sequence 2, Appli	PCT-US95-15781-2	5	184	31.0	403	28

US-08-240-124-2

Sequence 2, Application US/08240124

Patent NO. (51653)

GENERAL INCOMENSE A

APPLICANT: EBECKNANN, M. P.

APPLICANT: EBECKNANN, M. P.

APPLICANT: EBECKNANN, M. P.

TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: A

ADDRESSEE: IMMUNEX CORPORATION

STREET: SLIUNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

CITY: SEATTLE

STATE: MASHINGTON

COUNTRY: SAPILE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: APPLE APPLE MACHINGS

COUNTRY: APPLE APPL

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; MOLECULE TYPE:
US-08-453-943-2
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                                                                                                                                                                    Gaps
                                                                                      1 MAAAPLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                              181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                               ;
                            Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                           Indels
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                       100.0%; Score 1301; DB 1; 100.0%; Pred. No. 2.7e-128;
                                                         0
                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Microsoft Word for Apple, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-A0C-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-A0C-1993
ATTORNEY AGENT INFORMATION:
NAME: SEESE, KATHRYN A,
RECISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : IMMUNEX CORPORATION
51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08453943 Patent No. 5738844 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 587-0430
(206) 233-0644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                    Query Match 100.
Best Local Similarity 100.
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 51 UNA CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98101
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                                                                                                                                                                                                                                                                                                                                            1 MAAAPLLLILLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                               Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BERETTI, DOUGLAS P.
APPLICANT: BERETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
ADDRESSE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/057 *** FILING DATE:
                                                                             Score 1301; DB 1;
Pred. No. 2.7e-128;
                                                                                                                          ;
0
                                                                             Query Match 100.0%; Score 1301; Best Local Similarity 100.0%; Pred. No. 2.7 Matches 238; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09057121 Patent No. 5969110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WASHINGTON
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61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                Length 238;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08299567
Patent No. 574703
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Regeneron Pharmaceuticals, Inc.
STRRET: 777 Old Saw Mill River Road
CITY: Tarrycown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                              100.0%; Score 1301; DB 4;
100.0%; Pred. No. 2.7e-128;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPILING DATE: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1261; DB 1;
Pred. No. 4e-124;
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NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFRENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                  Matches 238; Conservative
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Best Local Similarity 97.9
Matches 233; Conservative
                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-358-734-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-299-567-5
                                                                                                                                   Best Local Similarity
         amino acid
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                                                                                                                                                Gaps
                                                                                                                                                                             1 MAAAPLILLILLIVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
                                                                                                                                              Indels
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                                                                                                      100.0%; Score 1301; DB 2;
100.0%; Pred. No. 2.7e-128;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AGC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AGC-1993
ATTORNEY AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/240,124
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09358734 Patent No. 6274117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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756822
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                                                                                                                         Best Local Similarity 100.0
Matches 238; Conservative
                              , MOLECULE TYPE: protein US-09-057-121-2
amino acid
                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101
               TOPOLOGY:
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US-09-358-734-2
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                                                                                                        Query Match
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113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172
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Best Local Similarity 50.5
Matches 96; Conservative
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; MOLECULE TYPE: protein
US-08-308-814-2
                                 171 SHSGEKPVPT 180
                                                              173 LYEAPEPIFT 182
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STATE: MA
COUNTRY:
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                                                                            61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                         121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SINDYLDIYCPHY-----GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNOHLRREGYTVOVNVNDYLD 60
                                                                                                                                                                                    2 AAAPLILILILVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 437; DB 1;
Pred. No. 5.4e-38;
5; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY APPLICATION: 800
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50.5%;
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amino acid
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Best Local Similarity 50.5%
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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US-08-455-001-2
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60 SINDYLDIYCPHY-----GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.6%; Score 437; DB 4;
50.5%; Pred. No. 5.4e-38;
ive 25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(txt)
CURRENT APPLICATION NATA:
FILLING DATE: 19-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/308,814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: 36.709
TELEFONMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
Sequence 2, Application US/08308814 Patent No. 6268476
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us-09-733-756-2.rai

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08920440B
Patent No. 5919905
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 287
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INPORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 amino acids
                                                            Best Local Similarity 50.5
Matches 96; Conservative
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                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAAPLILILILVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
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                                    EPH Receptor Ligands, and Uses Related Thereto
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50.5%; Pred. No. 5.4e-38;
tive 25; Mismatches 47.
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APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR APPLICATION NUMBER: 08/538,709
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1995-10-03
PRIOR FILING DATE: 1994-10-05
PRIOR PILING DATE: 1994-10-05
SOFTWARE: PAPLICATION NUMBER: 08/318,393
PRIOR FILING DATE: 1994-10-05
SOFTWARE: PALENTIN VET: 2.1
                                                                                                                                                                                                                                                                 NAME: Vincent, Matthew P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                TITLE OF INVENTION: EPH Receptor Lightee OF INVENTION: Thereto NUMBER OF SEQUENCES: 5 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-009-609-324A-10

Sequence 10, Application US/09609324A

Patent No. RE37582
                                                                                                                                                                                                                                                                                                                                                                                                                         : 209 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.69
Best Local Similarity 50.59
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-11869-2
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GENERAL INFORMATION:
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ORGANISM: LERK-6
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                                                                                                                                                                          SOFTWARE
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                                                                                2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 18; Gaps
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                                                                                                         18;
33.6%; Score 437; DB 1; Length 213; 50.5%; Pred. No. 5.6e-38; ive 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.6%; Score 437; DB 2; Length 213; Best Local Similarity 50.5%; Pred. No. 5.6e-38; Matches 96; Conservative 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPPY disk
COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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US-09-173-133-10
                                                                                                                                                                                                                                                                   STATE: W. COUNTRY:
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                               113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T_170
---GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116
                                                     54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINDYLDIYCPHY-----GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 437; DB 4; Length 213; 50.5%; Pred. No. 5.6e-38; Live 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PattentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/09/173,492
                                                                                                                                                                                                                                                                                           APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        Sequence 10, Application US/09173492
Patent No. 6194172
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Henry, Janis C.
REGIETRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 213 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.6%
Best Local Similarity 50.5%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-173-492-10
                                                                                                          171 SHSGEKPVPT 180
                                                                                                                                               177 LYEAPEPIFT 186
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
                                                                                                                                                                                                                      US-09-173-492-10
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113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 437; DB 4; Length 213; 50.5%; Pred. No. 5.6e-38; Live 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,133
             Parent No. 622447
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    E: Immunex Corporation
51 University Street
Sequence 10, Application US/09173133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %5-08-455-001-4
; Sequence 4, Application US/08455001
; Patent No. 5795734
; GENERAL INFORMATION:
; APPLICANT: Flanagan, John G.
; APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 213 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Henry, Janis C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-173-133-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 SHSGEKPVPT 180
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177 LYEAPEPIFT 186
                                                                                                                                                                    STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                             98101
                                                                                                                                                      ADDRESSEE:
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122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
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                                                                                                                                                                                                                                                                                                                                                                                                       3 AAPLLILLLUVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY
                                                                                                                                                                                                                                                                                                                       Length 200;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                     32.4%; Score 421; DB 5;
47.5%; Pred. No. 2.4e-36;
Live 29; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTE: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
TOR ADDITO: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROR APPLICATION 1939
APPLICATION NUMBER: 08/330128
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, TIMOCHAY
ERFERRNCE/POCKET NUMBER: 36,700
REFERRNCE/POCKET NUMBER: 36,700
REFERRNCE/POCKET NUMBER: 320C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,225.8674
TELEPHONE: 415,225.8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08442248 Patent No. 5759863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
          Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                86; Conservative
                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-11869-4
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Matches 86; Conserva
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US-08-442-248-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AAPLLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related TITLE OF INVENTION: Thereto NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related TITLE OF INVENTION: Thereto NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.4%; Score 421; DB 1; Best Local Similarity 47.5%; Pred. No. 2.4e-36; Matches 86; Conservative 29; Mismatches 50,
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1955
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
FLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9511869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 200 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-455-001-4
                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                       USA
                                                                                                                              Boston
                                                                                                                                                              COUNTRY: US
ZIP: 02109
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PCT-US95-11869-4
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11;
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                                                                                                                                                                                                                                                                                                  181 LPOFTMGPNVKINVLEDFE------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                             8 LLLLLVPVPILLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                           47;
                                                                                          Query Match 31.9%; Score 415.5; DB 1; Length 228; Best Local Similarity 39.5%; Pred. No. 1.1e-35; Matches 98; Conservative 37; Mismatches 66; Indels 47
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-442-248-4
                                                                                                                                                                                                                                                                                                                                                       229 AFFLMTFL 236
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Search completed: July 13, 2002, 10:45:32 Job time: 3112 sec

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July 13, 2002, 09:49:45; Search time 57.73 Seconds (without alignments) 457.917 Million cell updates/sec
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1 MAAAPLLILLLLVPVPLLPL......REHLPLAVGIAFFLMTFLAS 238
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                            Title:
Perfect score:
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10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human hek-L protei	Rob transmembrane	Mouse EDH recentor	Amino acid segment	avioa 3-888.I demin	Coperb remind levon	Chicken EPH recent	Amino acid seguenc	Human AL-1. a liga	Lerk-7 profein. H	HEK4 binding prote
RIES						'n	9	···	. 2	. ~	7	7	4	9	2
SUMMARIES			ID		AAR/148	AAR8260	AAR94766	AAW7100	AAY0682	ABG2783	AAR9476	AAW7100	AAR97854	AAW0258	AAW00035
			DB	1 1	9	16	17	19	20	22	17	19	17	17	11
			e Match Length DB 1	1 (	738	234	209	209	213	335	200	200	228	228	228
	ф	Query	Match	1 0	100.0	97.3	33.6	33.6	33.6	32.8	32.4	32.4	31.9	31.9	31.9
			Score	1 700	1301	1266	437	437	437	426.5	421	421	415.5	415.5	415.5
		Result	No.		-	2	٣	4	S	9	7	80	6	10	11

- r - r - c - c - c - c - c - c - c - c	eck receptor bindi Human PRO202 prote Human pancreatic c Truncated eck rece Truncated eck rece	2 2 2 2 2 2	Human hek-L protei LERK-6 exon polype Amino acid sequenc Human secreted pro EPH family ligand Human transmembran AL-2-short (AL-2s) Human cytokine Ler	NLERK2 ligand for AL-21.00g (AL-21) Ephrin-B2-Ephrin-B Ligand #2 for recepto Full length ligand for recepto Full length ligand Ligand for recepto Human hepatoma tra
AAW02587 AAR91283 AAY06820 AAR23895 AAR53634 AAR85604	AAWU4632 AAB50990 AAB54058 AAW18082 AAW18081	AAW18079 AAW18078 AAU12315 AAB50974 AAR94768	AAR71482 AAR91284 AAR06821 AAG03418 AAW17081 AAW3699 AAW31544	AAW10637 AAW33698 AAY66782 AAW06334 AAR94656 AAR94655 AAR94655
17 17 20 13 15 16	22 23 18 18 18	118 122 17 19	16 22 23 13 18 18	18 18 17 17 17
184 184 205 205 205	205 205 218 180 171	160 151 204 204 179	201 104 104 340 340 340	340 658 308 333 333
31.0 31.0 30.0 30.0	29.7 29.7 29.7 29.5 29.5	28.0 28.0 28.0 28.0 28.0	28.0 25.7 22.7 13.8 13.8 13.8	13.5 13.2 13.2 13.2
404 403 390 390 000	3 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	379.5 377.5 377.5 364.5	· m m m m m ~ ~	179 179 171.5 171.5 171.5 171.5
113 114 116	22 22 23 23	4000000	30 32 34 35 36 36	88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

### ALIGNMENTS

95WO-US04208

04-APR-1995;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 iycphynssgygpgagagggggaegyvlymvsrngyrtcnasggfkrwecnrphaphspi 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 kfsekfqrysafslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpvpt 180
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAAAPLILILLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytocoxic agents to particular leukaemia cells that express the hek see also AAR71482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ef1-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand; neurological disorder; identification; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "residue borders main conserved regions"
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1301; DB 16; Length 238; 100.0%; Pred. No. 8.1e-124; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eph transmembrane tyrosine kinase family ligand, Efl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "carboxy terminal hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPI-recognition tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..30
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                         Claim 21; Page 36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR82605 standard; Protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .235
             1995-106811/14.
                                                                                                                                                                                                                                                                                                                                 238 AA;
                             N-PSDB; AAQ85887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ef1-2; EHK1-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9527060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-1995
                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR82605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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Efl-2 (also known as EHK-IL) is an Eph transmembrane tyrosine kinase family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2 ends in a C-terminal hydrophobic sequence that appears to to be a recognition sequence allowing it to be GPI-linked and thus lacking in an intracellular domain. Efl-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligands which bind Eph family receptors - used in the diagnosis of
                                                                                                                     Maisonpierre PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1266; DB 16;
Pred. No. 2.8e-120;
0; Mismatches 0;
                                                                                                                   Goldfarb M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
21..209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
                                                                                                                                                                                                                                         Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR94766 standard; Protein; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse EPH receptor ligand Elf-1.
                                                                                                                     Gale N,
                                                                                                                                                                                                                                                                                                                                                                                                                                           97.3%;
98.3%;
                       94US-0327423.
94US-0222075.
94US-0229402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; transgenic animal.
                                                                94US-0299567
                                                                                          (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 234; Conservative
                                                                                                                                                                                                               neurological disorders
                                                                                                                   Davis S,
GD;
                                                                                                                                                         WPI; 1995-358635/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   234 AA;
                                                                                                                                                                        N-PSDB; AAT03883
                       21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
                                                                                                                   Aldrich TH,
Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR94766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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20-OCT-1998 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sindyldiycphy-----gaplppaermeryilymvngeghascdhrqrgfkrwecnr 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in the formation and maintenance of ordered spatial arrangements of olifferentiated tissue. It is the product of a CDNA clone (AAT15008) obtd. from an embryo mid- and hind-brain cDNA expression library. This cDNA is used for the rodm of recombinant Elf-1, which can be used to modulate prolifration, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                        Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 437; DB 17; Length 209; 50.5%; Pred. No. 3.6e-36; Live 25; Mismatches 47; Indels 2
                                                                                                     /note= "potential N-glycosylation site"
184
                                                                                    'note= "potential N-glycosylation site"
                                                                                                                                              /note= "potential N-glycosylation site"
                                                        /label= Core_sequence_motif
/label= Mat_protein
69..159
/label= Cys4_motif
35..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      dementia, tachycardia , etc.
                                                                                                                                                                                                                                                            95US-0393462.
94US-0308814.
                                                                                                                                                                                                                                 95WO-US11869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.68
Best Local Similarity 50.59
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                    Cheng H, Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-188446/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 lyeapepift 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 AA;
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT15008
                                                                      Modified-site
                                                                                                  Modified-site
                                                                                                                               Modified-site
                                                                                                                                                                          WO9609384-A1
                                                                                                                                                                                                                                  19-SEP-1995;
                                                                                                                                                                                                                                                            27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                     28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
               Region
                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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qq
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Mouse; EPH receptor ligand; Elf-1; mek-4; sek-Ap; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a mammalian EPH receptor ligand designated Elf-1. This ligand can bind to both mek 4 and sek AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzhenier's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "potential N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 35.166 /note= "contains core sequence motif"
                                                                 Amino acid sequence of a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 69..159 // Note= "contains a Cys4 motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21..209 /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2A; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0393462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheng H, Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-466665/40.
N-PSDB; AAV42926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5795734-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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NAME OF THE PROPERTY OF THE PR
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7;

Gaps

22;

Indels

33.6%; Score 437; DB 19; 50.5%; Pred. No. 3.6e-36; ative 25; Mismatches 47;

Query Match Best Local Similarity 50.5% Matches 96; Conservative

AAW71006 standard; Protein; 209 AA.

AAW71006

ò Db ò qq AAW71006

Length 209;

;

18; Gaps

52; DB 20;

33.6%; Score 437; DB 20; 50.5%; Pred. No. 3.7e-36; ive 24; Mismatches 52

Query Match
Best Local Similarity 50.5%,
Matches 96; Conservative

Length 213; Indels 63

54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112

2 AAAPLL-LLLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53 

g

g

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171 SHSGEKPVPT 180

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117

g

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113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T

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The invention relates murine and human LERK-6 polypeptides that bind to hekkelk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the chek or elk receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological classases, either chronic or acute. LERK-6 may be employed in treating neural garding may be administered to a mammal to exert a trophic or addition, they may be administered to a mammal to exert a trophic conducting quality assuance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the prevents and the prevent sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                              LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity.
                                                                54 NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                2 AAAPLLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV
                                                                                                                                                                                                                                                                                                     AAY06822 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 42; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US17772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0920440.
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Human LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-243567/20.
                                                                                                                                                                                         171 SHSGEKPVPT 180
                                                                                                                                                                                                                         173 lyeapepift 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX32767
                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerretti DP;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 58196; 103pp; English.
                                                                                                                                                                                                                  Novel human diagnostic protein #27828.
                                                                                                        ABG27837 standard; Protein; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
                                                                                                                                                                               (first entry)
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177 lyeapepift 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                               18-FEB-2002
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                                                                                                                                           ABG27837;
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human LERK-6 polypeptide.

213 AA;

Sequence

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Best Loca
Matches
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                              60 DIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHS 119
                                                                                                                                                                              119 PIKFSEKFORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHS 173
                                                                                                                                                                                                                                                      |:||||||| :: ||||:|| | ||:||||:
| Plkfsekfqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigv 277
                                                                                                                                                                                                                                         174 GEKPVPTLPQFTMGPNVKINVLEDFE------GEN-PQVPKLEKSISGTSPKREH 221
                                                                                                                     Gaps
                                                                                                                                  1 MAAAPLLLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYL 59
                                                                                                  DB 22; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                               tachycardia; therapy;
                                                                                                                   Indels
                                                                                                32.8%; Score 426.5; DB 22; 39.2%; Pred. No. 7.8e-35; 1ve 39; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Cys4_motif
33.157
/label= Core_sequence_motif
                                                                                                                                                                                                                                                                                                                                                                                                               dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                        AAR94767 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                            Chicken EPH receptor ligand Elf-1.
                                                                                                                                                                                                                                                                                                                                                                                                              receptor ligand; d
transgenic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0308814
                                                                                              Query Match 32.8%
Best Local Similarity 39.2%
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                            222 LPLAVGIAFFLMTFL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheng H, Flanagan JG;
                                                                       335 AA;
                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1995;
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19-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                              EPH
                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis;
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                                                                       Sequence
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Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.
                                                                                                                                                                                                                                                          chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 cphyee-----plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                               the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15009) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.4%; Score 421; DB 17;
47.5%; Pred. No. 1.4e-34;
ive 29; Mismatches 50;
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Misc-difference 61.150
/note= "contains a Cys4 motif"
Misc-difference 35.157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of an avian Elf-1 protein.
                                                                                                                                                                                                    Claim 1; Page 88-89; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW71007 standard; Protein; 200 AA.
                                                                                                                                           dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95us-0455001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
WPI; 1996-188446/19.
N-PSDB; AAT15009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AA;
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1996-239448/24.
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                 Modified-site
                                                  Modified-site
                                                                                                                                                                WO9613518-A1
                                                                                  Binding-site
                                                                                                                                                                                                            26-OCT-1995;
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                                                                                                                                                                                         The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates receptor ligands, B61 and LERK-2. The Elf-1 protein modulates of liferentiation and survival of EPH receptor-expressing by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increases neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of heaptocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 aaallaaivgvcv----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy 60
                                                                                                                        Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL-1; REK7; eph-related tyrosine kinase receptor; ligand; neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                ; Score 421; DB 19;
; Pred. No. 1.4e-34;
29; Mismatches 50;
                                                                                                                                                                    Claim 1; Columns 75-78; 53pp; English.
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 95US-0455001.
94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                                                32.4%; 47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
                                            HARD ) HARVARD COLLEGE.
                                                                    Cheng H, Flanagan JG;
                                                                                        WPI; 1998-466665/40.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                200 AA;
                                                                                                     N-PSDB; AAV42927
31-MAY-1995;
19-SEP-1994;
27-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                          ormation
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Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related tyrosine kinase receptor REK7 (AAR97853). Its amino acid sequence was deduced from a cDNA clone (AAT18897) isolated from a human foetal brain cDNA library. Recombinant, mature AL-1 can be produced in transformed host cells. It may be useful in promoting the development, maintenance or regeneration of neurons in vivo, and can be utilised in methods for the diagnosis and/or treatment of neurological disorders. It can also be used to promote or enhance angiogenesis. Antegonists and agonists of AL-1, as well as antibodies raised against AL-1, also have therapeutic applns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LPQFTMGPNVKINVLEDFE------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  des-----ypedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%; Score 415.5; DB 17; Length 39.5%; Pred. No. 6.1e-34; ive 37; Mismatches 66; Indels
                  37. 39
/label- Glycosylation
/note- "potential N-glycosylation site"
                                                                                                      162..164
/label= Glycosylation
/note= "potential N-glycosylation site"
/label= GPI
                                                                                                                                                                                                                                                              /note= "potential attachment site for
                                                                                                                                                                                                                                                                                              glycophosphatidyl-inositol"
                                                                                                                                                                                                                                                                                                                                                  /label= Hydrophobic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ====:::
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 54; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US14016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0486449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0330128
                                                                                                                                                                                                                                                                                                                          214..228
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Best Local Similarity 39.5
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caras IW, Winslow JW;
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The present sequence is that of human Lerk-7 protein. Lerk-7 is predicted to be anchored to the cell surface via 91ycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the exposed C-terminal amino acid of the processed mature protein, usually after cleavage upstream, often about 10-12 amino acids, of the N-terminus of the hydropholic domain. Lerk-7 coding sequence (AAT32569) was isolated using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for conjunction with elk, hek and eck receptors. They can also be used for the Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human Lerk-7 cytokine - which binds to cell surface receptors elk, hek and eck, useful for delivering agents to cells or for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                    "C-terminal stretch of hydrophobic residues"
                                                                                                                       Lerk-6; hek; elk; cell surface receptor; culture; reagent;
neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
Lerk-7; probe; cytokine.
                                                                                                                                                                                                                                                                                             /label= extracellular_receptor-binding_domain
                                                                                                                                                                                                                                                                                                                                                                               /label= GPI_attachment_site
                                                                                                                                                                                                                                                     1..228
/label= precursor_protein
                                                                                                                                                                                                                                        /label= signal_peptide
                                                                                                                                                                                                                                                                                                                            spacer_region
                                                                                                                                                                                                            Location/Qualifiers
             AAW02586 standard; Protein; 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 37-38; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US15781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0396946.
94US-0351025.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                         134..183
/label= sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-287171/29.
N-PSDB; AAT32699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 AA;
                                                                                              Lerk-7 protein.
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      WO9617925-A1
                                                                    28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-1996
                                         AAW02586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                            Key
Peptide
                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                     Region
AAW02586
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Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates HEK4 and ECK receptors. Its amino acid sequence was deduced from a cDNA clone (AAT34292) isolated from a human placenta cDNA library. Expression vectors and host cells can be used for the prodn. of biologically active HEK BP. It is useful for modulating the growth and/or differentiation of EpH sub-family receptor-bearing cells, esp. in liver, Kidney, lung, skin or neural tissues. It can be used to treat neural system disorders and in the regeneration of
                                                      67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                         126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                            118 fqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr--- 173
                                                                                                                                                                         181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to modulate growth and differentiation of, e.g. liver and kidney cells, and to treat cancer and nervous system disorders
               LLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEK4 binding protein; HEK4 receptor; EPH-like receptor; protein tyrosine kinase; ligand; growth; differentiation; cancer; nervous system disorder; therapy; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..19
/label= Sig_peptide
20..228
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      AAW00035 standard; Protein; 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 39-40; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US01079.
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                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            HEK4 binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bartley TD, Fox GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-362633/36.
                                                                                                                                                                                                                                   229 AFFLMTFL 236
                                                                                                                                                                                                                                                               218 llfilami 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT34292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9623000-A1
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                                                                                                                                                                                                                                                                                                                                                                    AAW00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                            RESULT
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11;

Gaps

47;

Length 228; Indels

31.9%; Score 415.5; DB 17; 39.5%; Pred. No. 6.1e-34; Live 37; Mismatches 66; 1

Query Match
Best Local Similarity 39.59
Matches 98; Conservative

184 AA:

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and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a murine cytokine, Lerk-6, encoded by AAF32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use as a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see AAF32699). The Lerk-7 gene
                                                                                                                                        67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                               126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                             6 eds-----vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek 117
                                                                                                                                                                                                                                    Gaps
                                                                                                 8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                              - which binds to cell surface for delivering agents to cells or
                                                                                                                                                                                                                                                                                                                                                                                                              hek; elk; cell surface receptor; culture; reagent; disorder; injury; delivery agent; diagnostic; therapeutic;
                                                                                                                                                                                                                     181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI
 tissues. Antagonists are useful for cancer can also be used to raise antibodies.
                                                                                47;
                                                              Length 228;
                                                                                Indels
                                                            DB 17;
                                                                   5.1e-34;
hos 66;
                                                           31.9%; Score 415.5;
39.5%; Pred. No. 6.1e
ilve 37; Mismatches
                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human Lerk-7 cytokine receptors elk, hek and eck, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 35; 49pp; English.
                                                                                                                                                                                                                                                                                                                                AAW02587 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0396946.
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lerk-7; probe; cytokine
 depleted 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-287171/29.
                                                                    Similarity
                              228 AA;
                                                                                                                                                                                                                                                            229 AFFLMTFL 236
                                                                                                                                                                                                                                                                                218 llfilami 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT32700.
                                                                                                                                                                                                                                                                                                                                                                                          Lerk-6 protein.
                                                                                                                                                                                                                                                                                                                                                                      28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cerretti DP;
 or
                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1996
          treatment.
                                                          Query Match
Best Local S
Matches 98
                              Sequence
                                                                                                                                                                                                                                                                                                                                                    AAW02587;
 damaged
                                                                                                                                                                                                                                                                                                                                                                                                              Lerk-6;
                                                                                                                                                                                                                                                                                                                                                                                                                         neuron;
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                                                                                                                                                                                                                                                                                                              RESULT
2223
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82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                                                                                                                                             Gaps
                                                                                              81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The LERK-6 polypeptide encoded can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by contact with the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hek; elk; cell surface receptors; culture; reagent;
disorder; injury; delivery agent; diagnostic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to hek
                                                                                                                      28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG
                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated DNA encoding cytokine designated LERK-6 which binds and elk cell surface receptors – useful for drug delivery and
  Length 184;
                                                Indels
                                                                                                                                                                                                                                                                                                    141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
31.0%; Score 403; DB 17; 50.6%; Pred. No. 8.5e-33;
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR91283 standard; Protein; 184 AA.
                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US12779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-209575/21.
  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LERK-6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1995;
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                                             82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR91283;
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184 AA;

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                                                                                               82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                                             Gaps
                                               28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
                                                            16;
31.0%; Score 403; DB 17; Length 184; 50.6%; Pred. No. 8.5e-33; ive 24; Mismatches 40; Indels 16
                                                                                                                                                 141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                              Similarity 50.6
32; Conservative
                       82:
 Query Match
                       Matches
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AAY06820 standard; Protein; 184 AA.
         24-JUN-1999 (first entry)
              Murine LERK-6 polypeptide.
      AAY06820;
AAY06820
ID AAY0
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LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity.

Mus sp.

WO9910495-A1. 04-MAR-1999.

98WO-US17772. 27-AUG-1998;

97US-0920440. 29-AUG-1997;

(IMMV ) IMMUNEX CORP.

Cerretti DP;

WPI; 1999-243567/20. N-PSDB; AAX32761. New cytokine designated LERK-6

Claim 6; Page 37-38; 46pp; English.

The invention relates murine and human LERR-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK enuclaic acid sequences are used for the recombinant production of the proteins. LERR-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the neural growth, development and/or maintenance. LERR-6 can be used for treating disorders of neural tissue such as injury or neurological consucrations where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic conducting quality as be administered to a mammal to exert a trophic conducting quality selection under different conditions. The polypeptides can select be used as carriers for delivering agents attached to cells bearing the elk protein under different conditions. The polypeptides can be used as carriers for delivering agents attached to cells bearing the elk prices which a present sequence represents a nurine LERK-6 polypeptide.

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184 AA;
Sequence
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The B1 protein sequence was deduced from the cDNA sequence obtd. by screening a cDNA library from human umbilical vein endothelial cells with radiolabelled cDNA fragments derived from the 5' end of B61 DNA. The B1 protein has 205 residues (24 kD) comprising a signal sequence and hydrophobic N- and C- terminal regions. The B61 gene is involved in early inflammatory response and serves as a marker. It may be detected by probes or by antibody-based immunossay of biological fluids such as plasma. CSF or urine. These assays make it possible to predict a worsening in a disease process and allow the quantitative assessment of the magnitude of the inflammatory response. This information will allow the earlier admin. Of appropriate therapy, thereby shortening the disease process and limiting the patient's exposure to anti-inflammatory/immuno-suppressive therapy. B61 induction is rapid and profound, hence
                                                                                                                               82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                                                                                  Gaps
                                                                  28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
                                                                                                3 anadryavywnrsnprfqvsavgdgggytvevsindyldiycphy-----gaplppae
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barly inflammatory response; marker; antibody; therapy; induction;
lipopolysaccharides; cytokines; Interleukin-2; IL-2; INF.
                                    16;
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     Length 184;
                                    Indels
                                                                                                                                                                                                  141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                                                                                     31.0%; Score 403; DB 20; 50.6%; Pred. No. 8.5e-33; ive 24; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Early inflammatory response;
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Query Match 31.0 Best Local Similarity 50.6 Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                B61 protein sequence.
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it is easily detectable. The B61 response is highly specific to proinfilammatory stimuli, being only made by cells exposed to lipopolysaccharides or cytokines such as IL-2 and TNF and not growth factors or interferon.
                                                                                                                     Ouery Match 30.0%; Score 390; DB 13; Length 205; Best Local Similarity 41.8%; Pred. No. 2.1e-31; Matches 87; Conservative 21; Mismatches 76; Indels 24;
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Search completed: July 13, 2002, 10:44:47 Job time: 3302 sec

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C 18 22 22 23 23 24 24 25 8	updates/sec 27 28 28 29 29 29 30 31 32 32				AESULT 1 AL565095/C LOCUS DEFINITION ACCESION	KEYWORDS KEYWORDS SOURCE ORGANISM	a TITLE JOURNAL COMMENT	FEATURES	AL55505 AL533153 AL533153 AL533153 (AL53316 (AL572018 (AL572018 (AL572018 (AL572018 (AL572018 (AL573013 (AL57314 (AL573114 (AL57311) (AL573111) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311) (AL57311
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Score 873.8; DB 9;
Pred. No. 1.7e-109;
14; Mismatches 32;
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94.5%;
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://alllength.invitrogen.com"
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Catarrhini; Hominidae;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebra
Mammalia: Eutheria; Primates; Catarrhini; Homini
1 (bases 1 to 1030)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genosc
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3; Mismatches 12;
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AL563020 AL5. NFL003_NBC3 Homo sapiens cDNA clone CSODC027YP19 3 prime, mRNA sequence.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDnA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.
Location/Qualifiers
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/notew"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center B710 English Maryland 20850, USA Fax: (1) 301 610 Http://fullingqelifetech.com URL: http://fullingqelifetech.com (RL: 9 others
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                                                                                                                                                                        Indels
                                                                                                                                                  Query Match
43.6%; Score 760.8; DB 9;
Best Local Similarity 97.9%; Pred. No. 3.7e-94;
Matches 782; Conservative 8; Mismatches 6;
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                                                                                                       BASE COUNT
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dassa; 1 to 702)

2 (Dassa; 1 to 702)

3 (Dassa; 1 to 702)

4 (Dassa; 1 to 702)

5 (Dassa; 1 to 702)

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7 (Dassa; 1 to 702)

8 (Dassa;
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Adb_xref="taxon:9606"

/clone="linAcB:24779506"

/clone=lib="NCI_CGAP_Skn3"

/clone=lib="NCI_CGAP_Skn3"

/lab_host="PHIOB (TI phage-resistant)"

/note="Organ: skin: Vector: pCWV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.3kb. Library constructed by Life

Technologies. Note: this is a NCI_CGAP Library."
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602634316F1 NCI_CGAP_Skn3 Homo s
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

LLAMINOOI row; a column: 15

High quality sequence stop: 715.

Location/Qualifiers

1. 1013

/Organism="Homo sapiens"
/db_xref="IAAGE: 436038"
/clone="IAAGE: 436038"
/clone="I
                                                                                  BF969747 1013 bp mRNA linear EST 22-JAN-2001 602272160F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4360358 5',
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Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1013)
NHT-MCC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.7e-88;
0; Mismatches 37; Indels 6;
                                                                                                                                                  mRNA sequence.
BF969747
BF969747.1 GI:12336962
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Best Local Similarity 94.8%;
Matches 787; Conservative (
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                                                                                                                    DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                       ORGANISM
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TITLE
JOURNAL
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Query Match

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241 795

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="cS0blo126Y124"
/clone="cS0blo126Y124"
/clone="lb="LTI_NFL06_PL2"
/tissue_type="placenta"
/note="Vector: pCWVSpORT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.

a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com URL : http://tullength.lnvitrogen.com"

http://tullength.lnvitrogen.com"

y a 199 c 241 g 153 t 20 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       Score 625.4; DB 9 Pred. No. 8.4e-76;
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94.3%;
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Matches 706; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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                                    DB 10;
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                                 Score 687.8; DB Pred. No. 3e-84;
                                                           0; Mismatches
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AL572018.1 GI:12929883
                                39.5%;
99.6%;
                                              Best Local Similarity 99.6
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/clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" 1. .131
                                  Yokohama,
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/db_xref="GI:12861021"
/translation="DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTLLAS"
      Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohan Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/db_xref="taxon:10090"
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AL Nature 409, 685-690 (2001)
CE 5 (bases 1 to 1085)
RS AdachiJ. Alzawa.K., Akahira.S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Hanagaki,T.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Hanagaki,T.,
Hara,A., Hayatsu,M., Hill,D., Hiramoto,M., Hanagaki,T.,
Rato,H., Rawai,J., Kojima,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Rawai,J., Kojima,Y., Konno,H., Kouda,M., Kasukawa,T.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Schriml,L., Shibata, K., Shibata,Y., Shinaqawa,A., Shiraki,T.,
Tanaka,T., Tejima,Y., Toya,T., Yamanuka,I., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome_Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                           HTC 19-JAN-2002
                                                                                                                                                                                                                                                  diaphragm region
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus (strain:C57BL/6J) 12 days embryo embryonic body
between diaphragm region and neck cDNA to mRNA, clone_lib:RIKEN
full-length enriched mouse cDNA library clone:9430025D14.
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Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
AK020438 10 days embryo embryonic body between and neck cDNA, RIKEN full-length enriched library, clone:9430025D14:ephrin A3, full insert sequence.
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Carninci, P. and Hayashizaki, Y.
High-effictency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                              1514 tttggagaccgtaaaacaacagcgcccc 1542
                                                                                          TTTGGAGACCGTAAAACAACAGCGCCCCC 3
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13;

Web : www.genoscope.cns.fr

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1. G84

/organism="Homo sapiens"
//db_xerf="texton:9606"
/clone="CsCoxon:9606"
/clone="Lib="LII_NFL003_NBG3"
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/clone_lib="LII_NFL003_NBG3"
/fissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pcWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@ilfetech.com URL: http://fulllength.invitrogen.com"
46 a 203 c 199 g 4 t 42 others
  1 (bases 1 to 684)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genos

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                                                                                               496 atcgcactccggggagaagccggtccccactctcccccagttcaccatgggccccaatgt
                                                                                                                                                                                                              .
0
684;
Length
            31; Indels
35.3%; Score 615.6; DB 9; 89.3%; Pred. No. 1.8e-74; tive 42; Mismatches 31;
    Best Local Similarity 89.3%
Matches 609; Conservative
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EST 13-FE3-2001

684 bp mRNA linear EST 13-FE3-7 Homo sapiens cDNA clone CSODC027YP19 5

AL527972 LTI\_NFL003\_NBC3

AL527972

AL527972 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

AL527972.1 GI:12791465 prime, mRNA sequence AL527972

human.

ORGANISM

SOURCE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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181 AGACATATGCCCCCAGAGAGAGAGAATCGAAGCGTGGGAGGCACCCCCATTGCTCTCCTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE.4357493"
/clone="IMAGE.4357493"
/clone="IMAGE.4357493"
/clone="IMAGE.4357493"
/clone="Lib="NIH_MGC_84"
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/lab_host="DH10B (phage-resistant)"
/note="Corgan: adrenal gland; Vector: pcWV-SPORT6; Site_1:
Not!; Site_2: Sall; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

260 c 208 g 178 t
                                                                                                                                                        BF968137 825 bp mRNA linear EST 22-JAN-2001 602269124F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4357493 5',
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9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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541 GAAGATWAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAA 600
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                     35.2%; Score 614.4; DB 10; Length 826; 89.4%; Pred. No. 2.5e-74; Live 0; Mismatches 66; Indels 21;
                                                                    676 cttcctcatgacgttcttggcc 697
                                                                                     661 CTTCCTCMCGACGTATCTTGGC 682
                                                                                                                                                                                                       BF968137.1 GI:12335352
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BF968137
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nes 735; Conserv
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BF983120 804 bp mRNA linear EST 23-JAN-2001 602305829F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397263 5',
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1461
                                                                                     1164 ttcccctgtttacagcaataagcacgtcctccccccactcccacttccaggattgtgg 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1462 ggcccctcttttgtcttctgtgaagacaggacctatgcaacgcacaga----cactttt 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1517 ggagaccgtaaaacaacagcgcccctcccttccagccctgagccgggaaccatctccca 1576
                                                                                                                480
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyer Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. i column: 08
Plate: LLAM10097 row: i column: 08
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                               1577 ggaccttgccccccctatgtggtcccacctatcctcctgggccttttcaagtgc
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BG698896.1 GI:13966642
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32.5%;
Best Local Similarity 94.8%;
Matches 704; Conservative 0
                          mRNA sequence.
                  602703313F1
                                     BG698896
                                                                  human.
                                             VERSION
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Site_1: Not!, Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
erriched for full-length clones and constructed by Life
fechnologies. Note: this is a NIH_MGC Library."
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                                                                                                                                              DB 10; Length 804;
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                                                                                                                                            33.2%; Score 578.6; DB 1.
ilarity 94.0%; Pred. No. 1.8e-69;
Conservative 0; Mismatches 34
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Mannalia; Euthbria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 762)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov.

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Long through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM10691 row: j column: 03

High quality sequence stop: 762.

Ab ref="taxon:e8606"

/clone="Image:"Monda2"

/lab\_host="heliob (T1 phage-resistant)"

/lab\_host="heliob (T1 phage-resistant)"

/lab\_host="bellob"

/lab\_host="bell 762 bp mRNA linear EST 07-MAY-2001 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4800482 5', 11; ggccaaaaagggcagtgctcaggactccctggcccctggtacctttccctgactcctggt 1018 gggaggcaccccattgctctcctccaggggcagaacatggggaggggactagatgggca 1138 718 958 296 297 GGCCAAAAGGGCAGTGCTCAGGACTCCCTGG-CCCTGGTACCTTTCCCTGACTCCTGGT 355 13; Gaps 9 tggggggggagagatggggggggcttggaaggagcagggagcctttggcctctccaagg 899 ggacagccatgggtcccgggcggccttgtggctctggtaatgtttggtaccaaacttggg Length 762; Indels Score 566; DB 10; Pred. No. 9.4e-68; 0; Mismatches 26; ô

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human.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone=Lib="LTL_NFLO06_PL2"
/fissue_type="placenta"
/rissue_type="placenta"
/note="Vector: pcMvSPORT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetch.com URL : http://fulllength.invitrogen.com"
l61 a 297 c 278 g 156 t 10 others
                                                                                                                                                                                                                                                                                                                         902 bp mRNA linear EST 16-FEB-2001 AL546822 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI026Y124 5 AL546822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                           cccactcccacttccaggattgtggtttggattgaaaccaagtttacaagtagacaccc 1258
                                                                                                                                                                                             -GGAGGCACCCCCATTGCTCTCCTCCA-GGGCAGAACATGGGGAGGGACTAGATGGGCA 473
                                                   aggggcagcactgcctgcttccttccctgtttacagcaataagcacgtcctcctcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 31006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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Pred. No. 4.9e-66;
1; Mismatches 37
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Local Similarity 91.1%;
les 749; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 547)
11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
          387
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ctatctggatatttactgcccgcactacaacagctcgggggtgggccccgggggg---g
                                       508 g-gagaagccggtccccactctccccagttcaccatgggccccaatgtgaagatcaacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-r@mall.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence. BG499730
BG499730 GI:13461247
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BF953157.1 GI:12370432
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Best Local Similarity 97.9%;
Matches 466; Conservative (
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Fax: +55-11-2707001
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/lab_host="BulloB (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: policy organisms of policy organisms o
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                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML476 row: g column: 12
High quality sequence stop: 537.
Location/Qualifiers
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Pred. No. 7.3e-63;
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@fanage.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stopp: 414.
Location/Qualifiers
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/do ganism=Homo sapiens"

/db xref="taxon:9606"

/clone="IMAGE:2835980"

/clone="Inb="NcI_CGAP_Pan1"

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/lab_host="DH10B"

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Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT:

Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                              BE138904 420 bp mRNA linear EST 21-JUN-2000 xw97ell.xl NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2835986 3',
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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0; Mismatches 2; Indels 0
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                                                          180 GAGACCGTAAAAACAACGCCCCCTCCCTTCCAGCCCTGAGCCGGGAACCATCTCCCAG 121
360 TATATATAATGTACAGACAGACAGGTCCCTTCCCTCTTTAACCCCCTGACCTTTCTTGA 301
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Search completed: July 13, 2002, 09:10:59 Job time: 1839 sec

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116.4
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   July 13, 2002, 08:43:30 ; Search time 216.15 Seconds (without alignments) 13844.931 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum DB seq length: 200000000
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			Description		Eph transmembrane	Human hek-L protei	Human colon cancer	Human colon cancer	Human secreted pro	Human LERK-6 polyp	Chicken elf-1 cDNA	CDNA encoding an a	Mouse Elf-1 cDNA.
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			B		٥T	16	21	21	21	20	17	19	17
			Match Length DB ID		10/0	1037	715	257	358	642	783	783	1809
	ф	Query	Match		0.40	52.7	25.7	14.5	11.8	8.6	8.6	8.6	8.0
			Score	010	2.0.5	917.8	447.8	252.2	205.8	149.2	149.2	149.2	139.6
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The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis).
       gtgtccgcccctctaccccttcccccagtagggcactgtagtggaccaagcacgggg
                                                      agectagtgggcetagaecectectectagtggetagaagtggggeetgeacatacatet
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                                                                                                                                                                                                                                                                                                                                                                          cell surface; tyrosine kinase receptor; tumorigenesis;
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                                                                                                                                                                                                                                                                               AAQ85887 standard; cDNA to mRNA; 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
83..799
/*tag= a
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93US-0114426.
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                                                                                                                                                                                                                                                                                                                                                                                        immunogen; ss
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03-DEC-1993;
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                                                                                                                              The DNA encodes an Eph transmembrane tyrosine kinase family ligand designated Ef1-2. Ef1-2 is useful for identifying other ligands for Ehk-1. -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
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                                                                                                                                                                                                                                                     DB 16; Length 1070;
     Maisonpierre PC;
                                                                                                                                                                                                                                                   Score 949.2; DB 16; Length
Pred. No. 3.8e-181;
0; Mismatches 18; Indels
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 Goldfarb M,
                                                                                                           Disclosure, Fig 3; 58pp; English.
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   Gale
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al Similarity 97.0%;
976; Conservative
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It is also an immunogen for antibody production, as a reason, detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-Lalso binds the elk tyrosine kinase receptors.
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                       Length 1037;
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Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;
                       DB 16;
                      Score 917.8; DB 16;
Pred. No. 7.4e-175;
0; Mismatches 2;
                      52.7%;
99.8%;
                      Ouery Match 52.7
Best Local Similarity 99.8
Matches 919; Conservative
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libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
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                                                                                                                                                                                                                                                            probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
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                                                                                                                                                                                                                                                diagnosis; gene expression product;
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Hases K, Randazzo F, Kennedy GC, Pot D, Kassam
Hanac R, Crkvenjakov R, Dickson M, Drmanac S, L
Kita D, García V, Jones LW, Stache-Crain B;
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BP
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98US-0085537.
98US-0085696.
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Drmanac R,
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15-MAY-1998;
21-OCT-1998;
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21; Length 715;

Score 447.8; DB 2 Pred. No. 1.2e-80;

25.7%; 95.3%;

Query Match Best Local Similarity

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AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test of the differentially expressed gene product in a test cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for mammalian cell. The polynucleotides can also be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                              Polynucleotide library used to determine cancerous states of mammalian cells \cdot
 Crkvenjakov R, Dickson M, Drmanac
Garcia V, Jones LW, Stache-Crain
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                                                                                                  Claim 1; Page 216; 1097pp; English.
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  Drmanac R,
D, Kita D,
                                     WPI; 2000-126369/11.
               Leshkowitz D,
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                                                                                                                                                                                                                                                                                 411 aaaacaacaagcgcccctcccttccagcccttgagccgggaaccatctcccaggacctt 470
  Gaps
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Pot D, Kassam A;
                                                                                                                                                                                                                                                                                                                                                                                                                 1642 ctgtgactttcatactctgctctt--agtctaaaaaaaataaactggagataaaat 1696
                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer cell line polynucleotide sequence SEQ ID NO:153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; ss.
  7;
 18; Indels
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Giese K, Randazzo F, Kennedy GC,
  Mismatches
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98US-0085537.
98US-0085696.
98US-0105234.
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9958675-A2
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512;
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                                                                                                                                                                                                                                               1166 ecectgittacagcaataagcacgiccicciccccactcccacticcaggaitgiggit 1225
                                                                                 Gaps
                                                                                                                                                9
                                                                                                                                  0;
                                             Query Match
14.5%; Score 252.2; DB 21; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.6e-41;
Matches 254; Conservative 0; Mismatches 3; Indels 0;
Sequence 257 BP; 58 A; 74 C; 59 G; 66 T; 0 other;
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us-09-733-756-1.rng

98WO-US17772. 97US-0920440.

27-AUG-1998; 29-AUG-1997;

04-MAR-1999

WO9910495-A1.

(IMMV) IMMUNEX CORP

Cerretti DP;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are fitten obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been Datained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                   Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 3422; 71pp + CD-ROM; English.
                                         21-FEB-2000; 2000EP-0200610.
                                                                                99US-0122487.
                                                                                                                                                              Dumas Milne Edwards J,
                                                                                                                                                                                                        WPI; 2000-500381/45
                                                                                                                                                                                                                                P-PSDB; AAG03418
                                                                                                                       (GEST ) GENSET
                                                                                26-FEB-1999;
06-SEP-2000
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Sequence 358 BP; 74 A; 102 C; 122 G; 60 T; 0 other;

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                                                 gagtactactacatctccacgcccattcacaacctgcactggaagtgtctgaggatgaag 472
                                                                      131 gagaatcgctgtttctccacgcccactcacacctgcactggaagtgtctgaggatgaag 190
                                                                                                473 gigitegicigetgegeetecacategeacteeggggaggaggeeggteeecacteteeee 532
                                                                                                               cagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagaac 592
                                                                                                                                                               Gaps
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  DB 21; Length 358;
11.8%; Score 205.8; DB 21; Length 94.7%; Pred. No. 3.5e-32; Live 0; Mismatches 12; Indels
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Best Local Similarity 94.7
Matches 213; Conservative
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LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity; ss.
             AAX32767 standard; cDNA to mRNA; 642 BP.
                                                                                             polypeptide encoding cDNA.
                                                                  (first entry)
                                                                                         Human LERK-6
                                                                 24-JUN-1999
                                                                                                                                                                          Homo sapiens
                                        AAX32767;
AAX32767
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cogctcaagttctcggagaagttccagctcttcacgcccttctccctgggcttcgagttc 426

341 367

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The invention relates murine and human LERR-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERR-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the chancement, stimulation, proliferation or growth of cells expressing the neural growth, development and/or maintenance. LERR-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERR-6 may be employed in treating neurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the alk or hek cell surface receptor. The present sequence represents a new and the alk or hek cell surface receptor. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gatatttactgcccgcactacaacagctcgggggtgggccccgggggcgggaccggggccc 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 gcaggcgcggggggacgacggcggggggtacacggtggaggtgagcatcaatgactacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20; Length 642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 642 BP; 97 A; 247 C; 193 G; 105 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 149.2; DB Pred. No. 9e-21; 0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a human LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                       New cytokine designated LERK-6
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61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 61.8
29; Conservative
                                                                                                                                                                                                                                                                                  Claim 3; Page 42; 46pp;
                                                                                                                                                                                                        WPI; 1999-243567/20.
                                                                                                                                                                                                                       P-PSDB; AAY06822.
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Best Local Simi
Matches 329;
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A chicken cDNA clone (AAT15009) codes for a novel EPH receptor ligand, EBIf-1 (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from a day.3 chick embryo cDNA library using mouse EBIf-1 cDNA (SPA EBIF-1) in the breeding of transgenic animals, for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine and chicken EPH receptor ligand, {\rm Elf}\text{-}1 - useful in diagnosis and treatment of disorders associated with the {\rm Elf}\text{-}1 gene, e.g. dementia, tachycardia , etc.
                                                                                                                                                                  Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;
                                 Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;
                                                                                                                                                                            transgenic animal; ss; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 36; Page 87-88; 107pp; English.
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                 ВР
                                                                                             AAT15009 standard; cDNA; 783
                                                                                                                                                                                                                                                                                                                                                                                      95US-0393462
94US-0308814
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1471..1476
/*tag= f
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/*tag= a
86..688
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149..685
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686..783
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P-PSDB; AAR94767.
                                                                                                                                                  Chicken elf-1 cDNA
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                                                                                                                                 02-JUL-1996
                                                                                                                                                                                                                                                                                                            polyA_signal
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                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                            diagnosis;
                                                                                                                                                                                             Sallus sp
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                                                                                                                                                                                                              Key
5'UTR
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DB 17; Length 783;

8.6%; Score 149.2;

Query Match

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Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intraeclular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation; ss.
                                                                                            76 aaaccygcatycygtytactygaacayctccaaccaycacctycygcyayayyyctacac 135
                                                                                                            255
                                                                                                                                                                                                                                                                312
              Gaps
                                                                  109 gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgaccccggcaaagtgatctc 168
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                                                                                                                                                    136 cgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaacagctcggg
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                                                                                                                                                                                                                                                                                                                                             385 gigcaaccggcccgactccccagcggaccctcaagttctcagagaagttccagctctt
                                                                                                                                                                                                                                                                                                                                                                       373 cagogoottotototogggotacgagttocacgcoggcoacgagtactacatotocac
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               Indels
 Pred. No. 9.4e-21;
); Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding an avian Elf-1 protein.
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94US-0308814.
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86..688
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86..148
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Matches 276; Conservative
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19-SEP-1994;
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receptor ligand; dementia; tachycardia; gene therapy; transgenic animal; ss; ds.

Location/Qualifiers 1..264 /\*tag- a 255..893 /\*tag- b 265..324

/\*tag- c 325.891 /\*tag- d 892.1809 /\*tag= e 1471.1476 /\*tag= f

us-09-733-756-1.rng

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Murine and chicken EPH receptor ligand, {\rm Elf}-l -useful in diagnosis and treatment of disorders associated with the {\rm Elf}-l gene, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-188446/19.
P-PSDB; AAR94777.
                                                                   Mouse Elf-1 cDNA.
                                           02-JUL-1996
                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                           polyA_signal
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                                                                                          Elf-1; EPH
                                                                                                          diagnosis;
                   AAT15008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheng H,
                                                                                                                                                        Key
5'UTR
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       a
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                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                 The present sequence encodes an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-Ap. Elf-1 is a phosphatidylinostical linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERR-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing of linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERR-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended fransplantation), also therapeutically in increase neuron survival eg. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgcccggcaaagtgatctc 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 ggaccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacac 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 ggtgggccccgggggccgggggcccgggaggcggggcagagcagtacgtgctgtacat 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgaggggctacac 135
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                                                                                                           Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               8.6%; Score 149.2; DB 1
63.3%; Pred. No. 9.4e-21;
                                                                                                                                                              Claim 12; Columns 73-76; 53pp; English
  95US-0393462
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                        (HARD ) HARVARD COLLEGE
                                                 Flanagan JG;
                                                                         WPI; 1998-466665/40.
P-PSDB; AAW71007.
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 276; Conserv
  27-FEB-1995;
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Best Local Si
Matches 276;
                                                 Cheng H,
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95US-0393462. 95WO-US11869

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                                                                  A mouse cDNA clone (AAT15008) codes for a novel EPH receptor ligand, Elf-1 (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from an embryo mid- and hind-brain cDNA expression library using a receptor affinity probe technique with mek4-AP and sek-AP (AP = alkaline phosphatase) reagents. The cDNA is used for the prodn. of recombinant Elf-1, in the breeding of transgenic animals, for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 139.6; DB 17; Length 1809; ilarity 62.4%; Pred. No. 9.7e-19; Conservative 0; Mismatches 134; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;
Claim 36; Page 84-85; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 292; Conserv
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AAT15008 standard; cDNA; 1809 BP.

AAT15008 ID AAT1

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Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
       ---gagagggctacaccgtgcaggtgaacgtgaacgactatct 162
                          ggatatttactgcccgcactacaacagctcgggggtgggccccgggggccgggggcc 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding a mammalian Elf-1 protein.
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P-PSDB; AAW71006.
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27-FEB-1995;
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The present sequence encodes a mammalian EPH receptor ligand designated EIF-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of herman antificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
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Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LERK-6; hek; elk; cell surface receptors; culture; reagent; neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 gc-----gagaggetacaccgtgcaggtgaacgtgaacgtgaacgactatet
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                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 139.6; DB 19;
62.4%; Pred. No. 9.7e-19;
live 0; Mismatches 134;
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                                                              2A; 53pp; English.
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Best Local Similarity 62.4
Matches 292; Conservative
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                                                         Claim 12; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The LERK-6 polypeptide encoded by this sequence can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by contact with the polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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Best Local Similarity 70.9%; Pred. No. 4.4e-18;
Matches 219; Conservative 0; Mismatches 66; Indels 24;
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                                                                                                                                                                                      /product= LERK-6 protein fragment.
                                                                                                    Location/Qualifiers
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94US-0318393
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                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and elk cell
                                                                                                                                                                                                                                                                                                                                                         04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerretti DP;
                                                                                                                                                                                                                                                                                                 18-APR-1996
                                                                                                 Key
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RESULT

Qy Db Oy Oy Oy Oy

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The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the production of the proteins. LERK-6 polypeptides may be useful in the neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neural growth, they may be administered to a manmal to exert a trophic of neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                    LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 gagaggetacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgcact 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 at------ggggcgccgctgccgccggcggagcgatggagcact 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 acgigotgiacaiggigagocgcaacggctaccgcacctgcaacgccagccag---ggct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 314 BP; 51 A; 108 C; 104 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 135.4; DB 2
Pred. No. 4.4e-18;
0; Mismatches 66
AAX32766 standard; cDNA to mRNA; 314 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon sequence from human LERK-6 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 24; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cytokine designated LERK-6
                                                                                                                                                                              Exon sequence of human LERK-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.88;
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                                                                                                                      (first entry)
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Best Local Similarity
Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY06821
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  W09910495-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1997;
                                                                                                                   24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerretti DP;
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243 acgigotgitacaiggigagocgcaacggotacogcaccigcaacgccagccag---ggot
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                A fragment of murine Lerk-6 DNA was isolated by PCR for use as a probe identification of a human Lerk-7 gene (see AAT3269). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering proteins or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins or also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9a9a9gsctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgcact 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 gcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcccacact 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human Lerk-7 cytokine - which binds to cell surface receptors elk, hek and eck, useful for delivering agents to cells or for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                Lerk-6; hek; elk; cell surface receptor; culture; reagent;
neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
Lerk-7; probe; cytokine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 128.8; DB 17; Length 555;
Pred. No. 1.1e-16;
0; Mismatches 82; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 34; 49pp; English.
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0
                                                                                                               AAT32700 standard; cDNA; 555
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                                                                                                                                                  (first entry)
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Matches 222; Conservative
                                                                                                                                                                  Lerk-6 coding sequence.
                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-287171/29.
                                                    420 actacatct 428
                                                              P-PSDB; AAW02587
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                                                                                                                                                  28-NOV-1996
                                                                                                                                                                                                                       Mus musculus
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06-DEC-1994;
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300 tcaagcgctgggagtgcaaccggccgcaccgcacagccccatcaagttctcggaga 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LERK-6; hek; elk; cell surface receptors; culture; reagent; neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated DNA encoding cytokine designated LERK-6 which binds to hek and elk cell surface receptors - useful for drug delivery and
                                                                                                      The LERK-6 polypeptide encoded by this sequence can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                              420 actacatctccacgcccactcacaacct 447
                                                                                                                                                                                                                                                                                                                               359 actacatctctgccacacctcccaacct 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT14009 standard; cDNA; 555 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 33; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LERK-6 coding sequence.
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/*tag=
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05-OCT-1994;
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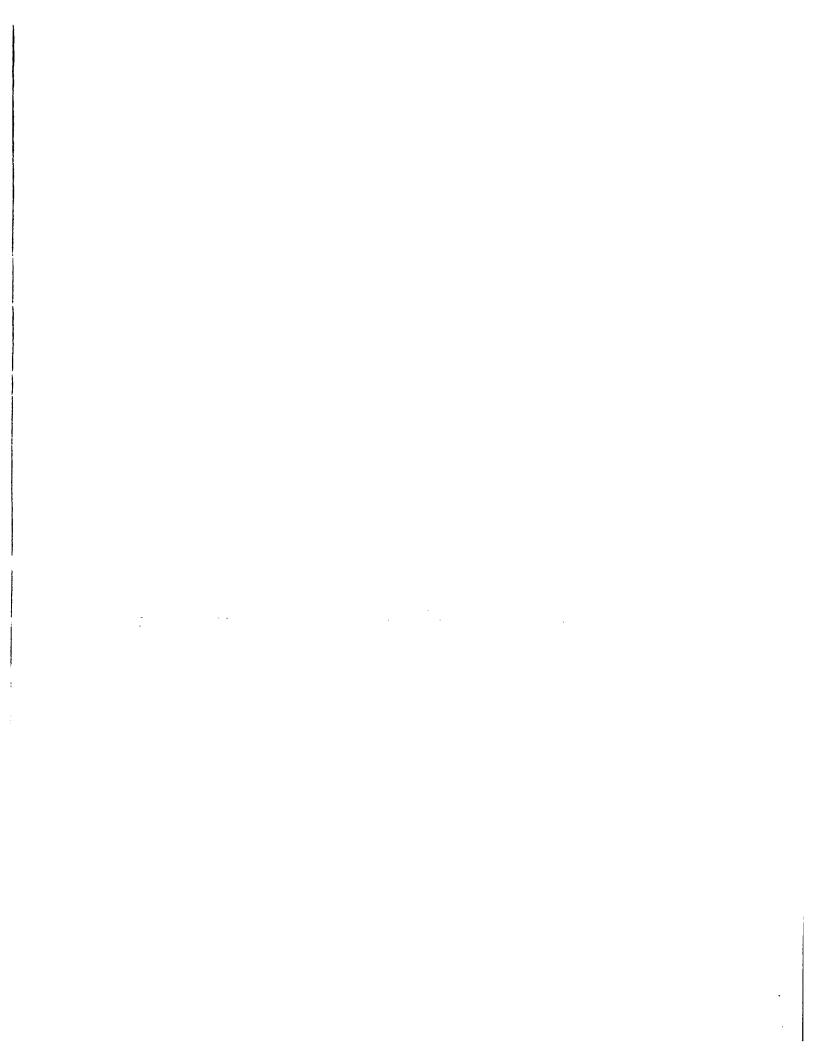
Score 128.8; DB 17; Length 555; Pred. No. 1.1e-16;

7.48; 67.78;

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                                                                                                                                                                                                                                                                                                                                                                                      LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity; ss.
                      179 acatcctgtacatggtgaatggtgagggccacgcctctgtgaccaccggcagggt 238
                                                                                                                                               300 tcaagcgctgggagtgcaaccggccgcacgcacagccccatcaagttctcggaga 359
                                                                                                                                                                                        Gaps
                                                                                                       82; Indels
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Murine LERK-6 polypeptide encoding cDNA.
                                                                                                                                                                                                                                420 actacatctccacgcccactcacaacct 447
                                                                                                                                                                                                                                             Claim 3; Page 37-38; 46pp; English.
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                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cytokine designated LERK-6
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  Conservative
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222;
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effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different condittions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a cDNA encoding a murine LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                        123 gagagggctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgcact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 acgigetgiacaiggigageegeaaeggelaeegeaeetgeaaegeeageeag---gget
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                                                                                                                                                                                                                                                                                                         24;
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                                                                                                                                                                              Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                       tch 7.4%; Score 128.8; DB 20; al Similarity 67.7%; Pred. No. 1.1e-16; 222; Conservative 0; Mismatches 82;
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Best Local Si
Matches 222
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Search completed: July 13, 2002, 09:53:34 Job time: 4204 sec



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Score Match Length DB

Result

Description

17722 Horn 21890 Horn 24292 Seq 01064 Seq 80871 Seq 64469 Seque 809 Seque 80	Omo s Mus Mus Dani 7 Rat	rus muscur 7 Sequence 3 Sequence 4 Sequence Gallus gall 5 Sequence	ΣΣ <u>0</u> · · · · · · · · · · · · · · · · · · ·	AC073818 Mus muscu U31204 Xenopus lae U31205 Xenopus lae U31205 Xenopus lea Y09668 D. rerio mRN U90666 Mus musculu AF317286 Gallus ga D38146 Mouse B61 m AR048795 Sequence I56902 Sequence I56902 Sequence I56902 Sequence II I88172 Sequence II
	9 HUMEFL2 2 AC104632 2 AC104327 5 AB051678 10 AY045577	AX3321 AF2097 AR1346 AR1520 CHKELF AR0237	292 11492 1147 2047 2047 203 319 319 319	AC0738 XLU312 XLU312 XLU312 DRTKLE DRTKLE AF3172 AF3172 AR1032 IS6902 IS6902 IS6902 IR8172 HUMB61
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## ALIGNMENTS

BC017722 1769 bp mRNA linear PRI 06-DEC-2001	Homo sapiens, ephrin-A3, clone MGC:21335 IMAGE:4397263, mRNA, complete cds.	DC017/22.1 GI:17389356 MGC.	human. Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1769) Strausberg, R.	Direct Submission	Submitted (U3-DEC-1001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC
RESULT 1 BC017722 LOCUS	DEFINITION	VERSION KEYWORDS	SOURCE ORGANISM		REFERENCE AUTHORS	TITLE	JOOKNAL	REMARK COMMENT

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                                                                             Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 27 Row: d Column: 19.

Location/Qualifiers
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human (Center, Stanford University School of Medicine, Stanford, (Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and R. M.
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Baylor College of Medicine

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Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                 Contact: hgsc-help@bcm.tmc.edu
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Mammalia; Euthenia; Primates; Catarrhini; Hominidae; Homo.

Muzny, D.M., Adams.C., Adio-Odoola, B., Ali-osman, F.R., Allen, C., Amaratunge, H.C., Are.J.R., Banks, T., Barbaria, J., Bentook, S.L., Amaratunge, H.C., Are.J.R., Banks, T., Barbaria, J., Bentook, S.L., Amaratunge, H.C., Are.J.R., Banks, T., Barbaria, J., Bentook, B. S.L., Bried, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Bento, P., Buhay, C., Burch, P., Burch, P., Burch, P., Burch, P., Burch, R.C., Claveland, C.D., Cox, C., Cleveland, C.D., Cox, C., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, T., Dederich, D.A., Delaney, R.R., Delagado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, R.J., Darger, H., Day, T., Dinh, H.H., Douthwaite, R.J., Darger, H., Day, T., Dubin, K.J., Erraguto, D., Flagy, N., Ford, J., Garzer, P., Erantz, P., Garelis, A., Garzer, P., Erantz, P., Garelis, A., Gao, J., Garzia, A., Garzer, P., Erantz, P., Garelis, A., Haris, C., Harris, C., Harris, K., Harris, C., Huber, J., Hulk, S., Homes, J., Homes, F., Howard, S., Huber, J., Hulk, S., Hume, J., Garsen, C., Katovi, C.J., Katovi, C.J., Li, J., J., Li,                                                                                                                                                                                                                                                                                                                                                    ACUZ1890 175826 bp DNA linear HTG 10-NOV-2000 HOMO sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE, 22 unordered pieces.
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On Nov 9, 2000 this sequence version replaced gi:9719697.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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SOURCE

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JOURNAL TITLE

COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                        Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.99329
Consensus quality: 144734 bases at least 040
Consensus quality: 162873 bases at least 030
Consensus quality: 169424 bases at least 020
Estimated insert size: 170770; sun-of-contigs estimation
Quality coverage: 0x in 020 bases; sum-of-contigs estimation
Quality coverage: 3.3x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                           21031: contig of 21031 bp in length 40475: contig of 19344 bp in length 40575: gap of unknown length 40575: gap of unknown length 57617: contig of 17042 bp in length 57717: gap of unknown length 75708: contig of 17991 bp in length 75808: gap of unknown length 89018: contig of 13210 bp in length 89118: gap of unknown length 100348: contig of 11230 bp in length 100488: gap of unknown length
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          Center clone name: RPII-498A2
------ Summary Statistics
Sequencing vector: M13; L08821
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Sequence 8
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Matches 976,
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                                       Score 1123.8; DB 2;
Pred. No. 7.7e-208;
0; Mismatches 2;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
               /clone="RP11-498A2"
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                                       64.5%;
99.8%;
                                      Query Match 64.5°
Best Local Similarity 99.8°
Matches 1125; Conservative
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Unclassified.
1 (bases 1 to 1070)
1 (bases 1 to 1070)
and Yancopoulos,G.D.
Method of enhancing the biological activity of Eph family ligands
Patent: US 5747033-A 8 05-MAY-1998;
Location/Qualifiers
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llarity 97.0%; Pred. No. 3.6e-174;
Conservative 0; Mismatches 18;
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8 from patent US 5747033.
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Beckmann, M. Patricia and Cerretti, D.P. Antibodes that bind hek ligands
Patent: US 5969110-A 1 19-OCT-1999;
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Beckman, M. Patricia. and Cerretti, D.P.
Cytokines that bind the cell surface receptor
Patent: US 5738844-A 1 14-APR-1998;
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Pred. No. 4.4e-168;
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Beckmann, M. Patricia and Cerretti, D.P.
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Beckmann,M.Patricia. and Cerretti,D.P.
DNA encoding cytokines that bind the cell surface receptor Patent: US 5516658-A 1 14-MAY-1996;
Location/Qualifiers
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Kozlosky, C.J., Maraskovsky, E., McGrew, J.T., VandenBos, T., Teepe, M., Lyman, S.D., Stinivasan, S., Fletcher, F.A., Gayle, R.B. III, Cerretti, D.P. and Beckmann, M.P.
Ligands for the receptor tyrosine kinases hek and elk: isolation of Oncogene 10 (2), 299-306 (1995)
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Human receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA, complete
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/codon_start=1
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/note="putative"
/124. .771
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/product="unnamed"
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VCCASTSHSGERFPVFTLPOFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHL
                                                                                                                                                                                                                                    HUMEFL2 Them sapiens (clone hEHK1-L) EHK1 receptor tyrosine kinase ligand (EFL-2) mRNA, complete cds.
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Davis,S., Gale,N.W., Aldrich,T.H., Maisonpierre,P.C., Lhotak,V. Pawson,T., Goldfarb,M. and Yancopoulos,G.D.
Ligands for EPH-related receptor tyrosine kinases that require membrane attachment or clustering for activity
Science (1994) In press
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 1.3e-126;
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* be preserved.  * 2056 2156 4 4236 * 4336 * 6527 * 6627																			
Qy         241 gtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgccagcca	361 gttccagcgcttccagcgcttcctctgggctacgagttccacgcggccaccagagtactt	Qy       421 ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgatggt 480         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0y 481 ctgctgcgcctccacatcgcactccggggagaagccggtccccactctccccagttcac 540	Oy 541 catgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaaccctcaggt 600	Oy 601 gcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacactgccctggc 660	QY 661 cgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgcccctcccctg 720	Qy         721 ggggggaagatggggc         738           Db         741 GGGGGGAGAGATGGGGC         758	RESULT 10	AC104632/c LOCUS AC104632 289579 bp DNA linear HTG 29-DEC-2001 DEFINITION Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT SFOIRENCE 72 increased viscose	ACCESSION AC104632 VERSION AC104632.2 GI:17998594 KEYWORDS HTG: HTGS PRAFT.	BEFERBNCE 1 (bases 1 (289579) Anthone 1. (bases 1 (289579) Anthone 1. (bases 1 (289579) BEFERBNCE 1 (bases 1 (289579) BEFERBNCE 1 (2895	TITLE Mus musculus BAC Clone rp23-368d24	REFERENCE 2 (bases 1 to 289579) AUTHORS Hua, A. and Roe, B.A.	OK 73019, USA.  COMMENT On Dec 29, 2001 this sequence version replaced gi:17861055.	Center: Department Of Chemistry And Biochemistry The University of Otlahoma	Center code:UNIN	* NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces	* 1S NOT KNOWN and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as	* runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will

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Location/Qualifiers

source

FEATURES

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Oy 572 gaagactttgagggagagaacctcaggtgcccaagcttgagaagagcatcagcgggacc 631
Db 184805 GAAGACTTTGAGGGAGAATCCCCAGGTGCCCAAGCTTGAGAAGAGCATCAGTGGGACC 184746
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                                                                                                                             Length 289579;
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Best Local 8
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SEQUENCE, 66 unordered pieces.
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Hua,A. and Roe,B.A.

Direct Submission
Submitsed (10-DEC-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Dec 24, 2001 this sequence version replaced gi:17439220.
Oy 1586 cetgeteaccetatgtggtccacctatcctctgggcettttcaagtgctttggctgt 1645 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 |
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 326750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                 DD 183768 GACTTTCATACTCTGCTCTTAGTCTAAAAAAAAAAAAAGCTGGAGATAAAAATA 183717
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The University Of Oklahoma
Center code:UOKNOR
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Unpublished
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AUTHORS
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TITLE
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g of 4151 bp in length
f unknown length
g of 8033 bp in length
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gap of unknown length
contig of 11968 bp in length
gap of unknown length
contig of 13352 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.8%; Score 642.2; DB 2; Length 81.2%; Pred. No. 2.3e-114; Live 0; Mismatches 164; Indels
                                                                                                                                                                                                                                                   of 10360 bp in length
                                                                                                                                                                                                                                                                                             of 10742 bp in length
unknown length
of 7863 bp in length
  in length
                      bp in length
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of 7605 bp in length
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of 8593 bp in length
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of 4567 l
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of 7682
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                                                                                                                                       of 5301
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rp23-295a4"
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210382: 0
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Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Teleostei; Euteleostei; Ostariophysi; [Vpriniformes; Cyprinidae; Danio. [Cypriniformes; Cyprinidae; Danio. [Hirate,Y., Mieda,M., Harada,T., Yamasu,K. and Okamoto,H. dentification of ephini-33 and novel genes specific to the midbrain-MHB in embryonic zebrafish by ordered differential display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRT 20-SEP-2001
195699 GTGGCTTTGGTAATGTTTGGTACCAAACCTGGGGGCTATAAA-GGCAGTGCTCAGGACTC 195757
                                                                                                                                  Db 196106 ATGTACAGACAGAGAGTCCCTTCCTTAACCTTGACCTTTCTGACTTCCCCTT 196165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196166 CCAGACTCAGACCCTTCCCCTACCAGGTTAGGCCCC----CCTTGGGACCCCCTGGCC 196221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1346 atgtacagacagacagatccettccctctttaaccccctgacttcttgacttccct 1405
                                                         9t9gctctggtaatgtttggtaccaaacttgggggccaaaagggcagtgctcaggactc
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                                                                                                                    cctggcccctggtacctttccctgactcctggtgccctctccctttgtcccccagagag
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Danio rerio mRNA for ephrin-A3, complete
AB051678
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Mechanisms of development, 107

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ROD 25-AUG-2001
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/product="ephrin A3"
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                                                                                                                                                            Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae;
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Minoz, J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A., Jimenez,E., Varas,A. and Zapata,A.G.
Expression and function of the Eph A receptors and their ligands ephilis A in the rat thymus
                                                                                                                                                                                                                                                                                      2 (bases 1 to 355)
Munoz.J.J., Alonso-C.L.M., Sacedon,R., Crompton,T., Vicente,A.,
Jimenez.E., Varas,A. and Zapata,A.G.
Direct Submission
Submitted (13-JUL-2001) Cell Biology, Complutense University of
Madrid, Av. Complutense, Madrid 28040, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Complutense University of , Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 cggggcccggaggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctacc 275
                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. .>355
/note="Eph-related receptor tyrosine kinases ligand"
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Pred. No. 5.7e-37;
0; Mismatches 37; Indels
                                                                         partial cds.

    .355
    /organism="Rattus norvegicus"
/db_xref="taxon:10116"

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                                                      355 bp
Rattus norvegicus ephrin A3 mRNA,
AY045577
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109 c 96
                                                                                                    AY045577.1 GI:15290522
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ilarity 87.7%;
Conservative
                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                        Unpublished
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POPTEPDYTLRPNIKIDDLDDYDNPEVPKLEKSISGSSPSRDRLLLTVASLLLIALSY
S"
                Construction (1938)

Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamoto, H.

Direct Submission
Submitted (24.NOV-2000) Yoshikazu Hirate, Brain Science Institute,
RIKEN, Lab. of Developmental Gene Regulation; 2-1, Hirosawa,
Wako-shi, Saitama 351-0198, Japan (E-mail:hirate@brain.riken.go.jp,
Tel:81-48-467-9713, Fax:81-48-467-9714)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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83-96 (2001)
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Pred. No. 4.5e-39;
0; Mismatches 155;
(1-2),
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                                                                                                                                                  /organism="Danio rerio"
/db_xref="taxon:7955"
550. 1209
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                                                                                                                                                                                               /gene="ephrin-A3"
550. .1209
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/gene="ephrin-A3"
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Best Local Similarity 68.0%;
Matches 399; Conservative
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E. Genomics 47 (1), 131-135 (1998)

E. Chases 1 to 2535)

Cerretti, D. P. and Nelson, N. Direct Submission

E. Submitted (11-MAR-1997) Molecular Biology, Immunex Corp., 51

University Street, Seattle, WA 98101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC39961.1"
/db_xref="G1:28439961.1"
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/translation="LRREGYTVQNNVNLSGERFORMVNLSGENPQYPKLEKS
ISGTSPRREHPLAVGIAFFLMTLLAS"
926. .1215
                   ROD 07-FEB-1998
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                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                  385 2535 bp DNA linear musculus LERK-3 (Epl3) gene, partial cds.
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Pred. No. 4.8e-33;
0; Mismatches 25;
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/db_xref="taxon:10090"
/chromosome="3"
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/number=4
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84.7%;
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/gene="Epl3"
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Matches 271;
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1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                               PAT 09-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1565 aaccatctcccaggaccttgccctgctcacctatgtggtccacctatcctcctgggcc 1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 0194629-A 2646 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
1.186
                                                                                                                                                                                                                                                       Sequence 2646 from Patent WO0194629. AX332137.1 GI:18122771
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/db_xref="taxon:9606"
34 c 61 g 41
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Query Match

54.5%; Score 949.2; DB 1; Length 1070;
Best Local Similarity 97.0%; Pred. No. 9e-186;
Matches 976; Conservative 0; Mismatches 18; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
TORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STEET: 777 old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: BLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/299,567
FLING DATE: 01-SEP-1994
ATTORNY APPLICATION: 435
         US-08 452-779-11
US-08-445-065-11
US-08-959-524-11
US-08-321-162-1
US-08-441-216-1
US-08-379-802-1
US-09-048-129-1
US-09-048-129-1
US-09-048-129-1
US-08-440-079-1
US-08-440-079-1
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US-08-453-943-3
US-09-057-121-3
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ER: REG 290
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Patent No. 5747033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REPRENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914.345-7400
TELEFAX: 914.345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
US-08-299-567-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                           1480
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                July 13, 2002, 08:42:45 ; Search time 53.99 Seconds
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6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-057-121-1
US-09-050-324A-9
US-08-920-04-0B-9
US-09-173-133-9
US-08-455-001-3
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US-08-308-814-1
US-09-609-134A-7
US-09-609-134A-7
US-09-173-42-7
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US-09-165-533-7
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US-08-920-440B-1
US-09-173-492-1
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                                                           nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

WASHINGTON

STREET: 51 UNIV CITY: SEATTLE STATE: WASHING?

Floppy disk

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

98101

RECEPTOR HER

TITLE OF INVENTION:

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                  ctacaacagctcgggggtgggcccggggccggggaccgggggccggagggggggagca 240
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                            Version 5.1a
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Pred. No. 2.4e-179;
0; Mismatches 2;
                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
              SYSTEM: Apple System 7.1
Microsoft Word for Apple,
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2814
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
TELERAX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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COMPUTER: Apple Macintosh
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ilarity 99.8%;
Conservative 0
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            OPERATING SYSTEM:
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Best Local Similarity
Matches 919; Conserv
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IMMEDIATE SOURCE:
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                            SOFTWARE:
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APPLICANT: BECKRANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE

Sequence 1, Application US/08240124 Patent No. 5516658 GENERAL INFORMATION:

US-08-240-124-1

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                                             APPLICANT: BECKRANN, M. P.
APPLICANT: BECKRANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: THAUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
STRIE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08453943
Patent No. 5738844
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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99.8%; Pred. No. 2.4e-179;
Live 0; Mismatches 2;
                                   Version
        OPERATING SYSTEM: Apple System 7.1
SOFTWARE: MICTOSOFT WORD for Apple, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY,AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: US 08/109,745
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY,AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 23,172
                                                                                                                                                                                                                                                                                                                                        RECERENCE/DOCKET NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-
TELECOMMUNICATION INFORMATION:
TELEFONE: (206) 233-0644
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.8
Matches 919; Conservative
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83..139
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140..796
COMPUTER: Apple NOPERATING SYSTEM:
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IMMEDIATE SOURCE:
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HYPOTHETICAL:
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FEATURE:
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US-08-453-943-1
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                                                                                                                                                                                                                                                     Sequence 1, Application US/09057121
Patent No. 5969110
GENERAL INFORMATION:
APPLICANT: CERRETIT, DOUGLAS P.
ATITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple E. stem 7.1
SOFTWARE: Microsoft Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/057,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : IMMUNEX CORPORATION
51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
                                                                                                                                                                                                                                                                                                                                                          901 acagccatgggtcccgggcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft WO-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-09-057-121-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.7%; Score 917.8; DB 2; 99.8%; Pred. No. 2.4e-179; iive 0; Mismatches 2;
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATORNEY/AGENT INFORMATION:
NAME: SEESE, KATHEYN A.
RECISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INCOMMER: 2814-C
                                                                                                                                                                                                 TELEFAN: (206) 587-0430
TELEFAN: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to HYPOTHETICAL: NO ANTI-SENCE
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nes 919; Conserv
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CLONE: hek-L A2
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FEATURE:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-09-057-121-1
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Best Local S
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                                                                                  GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09358734
; Patent No. 6274117
                                                                                                                                                                                                                                                                                                                                          ACAGCCATGGGTCCCGAGCAG 1017
                                                                                                                                                                                                                                                                                                                             901 acagccatgggtcccgggcgg 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 51
CITY: SEATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98101
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                                                                                                                                                                                                                                                                                                                    Length 1037;
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  32,172
ER: 2814-C
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                              MOLECULE TYPE: CDNA tO MRNA HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                              mat_peptide
140..796
                                                                                                              single
                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                            hek-L A2
                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 83...
                                                                                                 TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                    FEATURE:.
NAME/KEY:
                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                          Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149.2; DB 2;
Pred. No. 4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION ....
FILING DATE: 29 AUG-199/
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 587-0430
TELEFAX: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERICTICS:
LENGTH: 642 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08920440B
Patent No. 5919905
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
       gacatctactgcccgcactat-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..cuudgY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-CENTOR
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61.8%;
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Signal Peptide
1-90
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STREET: 51 Univ
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                               US-08-920-440B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-920-440B-9
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           781 agcctagtgggcctagacccctcctcccatggctagaagtggggcctgcaccatacatct
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09609324A

Patent No. RE37582

GRERAL INFORMATION

GRERAL INFORMATION

TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6

FILE REFERENCE: A7772

CURRENT APPLICATION NUMBER: US/09/609,324A

CURRENT FILING DATE: 2000-06-30

PRIOR FLLING DATE: 1997-08-29

PRIOR FLLING DATE: 1997-08-29

PRIOR FLLING DATE: 1997-08-39

PRIOR FLLING DATE: 1997-08-39

PRIOR FLLING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver: 2.1

FENCINE PATENTING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                               ACAGCCATGGGTCCCGAGCAG 1017
                                                                                                                                                                                                                                                                                                  acagecatgggteeegggegg 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: mat_peptide
; LOCATION: (88)..(639)
US-09-609-324A-9
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LOCATION: (1)
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US-09-609-324A-9
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USA
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                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-173-492-9
                                                              TOPOLOGY:
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                                                                                   88 GCCGGCGCAACTCGGACGCTACGCGTTCTACTGGAACCGCAGCAACCCCAGGTTCCAC 147
                                                                                                                  122 cgaga------gggctacaccgtgcaggtgaacgtgaacgtctatctg 163
                                                                                                                              148 GCAGGGGGGGGACGACGGGGGGCTACACGGTGGAGGTGAGCATCAATGACTACCTG 207
                                                                                                                                                                                                                                                           284 aacgccagccag---ggcttcaagcgctgggagtgcaaccggccgcacgcacagc 340
                                                                                                                                                                                                                                                                          307 GACCACCGCCAGCGCGCTTCAAGCGCTGGGAGTGCAACCGGCCCGGGGGGG 366
                      45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09173492
Patent No. 6194172
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Henry, Janis C.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98101
Matches 329;
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Patent No. 623247
CENERAL INFORMATION
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                         Score 149.2; DB Pred. No. 4e-22;
     6
                                                                                                        CDNA to mRNA
                                                                                                                                                                                                                                                                                         Query Match 8.6%;
Best Local Similarity 61.8%;
Matches 329; Conservative
                                                                                                                                                                                                       Signal Peptide
1-90
                                   LENGIH: 642 base pairs
TYPE: nucleic acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                        single
                                                                                      linear
                                                                                                                                                                                       11642
                                                                                                                                    ANTI-SENSE: NO FEATURE:
                                                                 STRANDEDNESS:
                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
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ATTORNEY/AGENT INFORMATION:
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60 State Street
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      686..783
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FEATURE:
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US-08-455-001-3
                                                                                                                                                                                                                                     COUNTRY:
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Pred. No. 4e-22;
0; Mismatches 158; Indels 45
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                     NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INPOREMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,133
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.6%;
Best Local Similarity 61.8%;
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                       CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                            Signal Peptide 1-90
                                                                                                                                                                                                                                                       LENGTH: 642 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                              single
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11642
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                                                                                                                                                                                                                                                                 TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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US-09-173-133-9
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76 aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacac 135
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                                                                                           APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwal-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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8.6%; Score 149.2; DB 1;
Best Local Similarity 63.3%; Pred. No. 4.2e-22;
Matches 276; Conservative 0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 227-7400
TELEFAN: (617) 227-7401
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-455-001-3
; Sequence 3, Application US/08455001
; Patent No. 5795734
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Mathew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1615 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-08-308-814-1
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                                                                                                99t9agccgcaacggctaccgcacctgcaacgccagcc--agggcttcaagcgctggga 312
                                                                                                                             325 GGTCAACTACGAGGGCCACGCGTCCTGCGACCACCGGCAGAAGGGCTTCAAACGTTGGGA 384
                                                                                                                                                                 gtgcaaccggcacgcacgcacagccccatcaagttctcggagaagttccagcgcta 372
                                                                                                                                                                               385 GTGCAACGGCCCGACCCCCAGGGACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTT 444
                                                                                                                                                                                                                               cagegeettetetetgggetacgagttecacgeeggeeacgagtactactacateteeac 432
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                                                                 ----GGAGCCGCTGCCCGCCGAGCGCATGGAGCGCTACGTCCTCTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
229 CGIGGAGGIGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 8.6%; Score 149.2; DB 5; Best Local Similarity 63.3%; Pred. No. 4.2e-22; Matches 276; Conservative 0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7401
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application PC/TUS9511869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              gcccactcacaacctg 448
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LOCATION:
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PCT-US95-11869-3
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FEATURE:
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PCT-US95-11869-3
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279 136 cgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaacagctcggg 195 255 312 125 GGTCAACTACGAGGGCCACGCGTCCTGCGACCACCGGCAGAGGGCTTCAAACGTTGGGA 384 gtgcaaccggccgcacgccccgcacagccccatcaagttctcggaagaagttccagcgcta 372 76 aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacac 229 CGTGGAGGTGAGCATCAATGACTGGACATCTACTGCCCTCACTACGA-----196 ggtgggccccgggggcgggaccgggggcccggaggcggggcagagcagtacgtgctgtacat 280 ------GGAGCCGCTGCCCGCCGCGATGGAGCGCTACGTACGTCTACAT ggtgagccgcaacggctaccgcacctgcaacgccagcc---agggcttcaagcgctggga Ligands, and Uses Related GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Li
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street SOFTWARE: ASCII(txt)
CURREWA PAPLICATION DATA:
APPLICATION UNHER: US/08/308,814
FILING DATE: 19-SEP-1994 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 1, Application US/08308814 Patent No. 6268476 TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:

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                                                                                                                        Length 1615;
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APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 CCGCCCTGCCCACGAATACTACTACTTCTCTGCCACCTCCCAACCT 470
                                                                                                                        Score 139.6; DB 4; Length Pred. No. 4.7e-20; 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 ccacgccggccacgagtactactacatctccacgcccactcacaacct 447
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COMPUTER: IBM PC COMPALIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
                                                                                                                             8.0%;
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                                                                                                                             Query Match
Best Local Similarity 62.45
Matches 292; Conservative
                                               sig_peptide
10..69
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MEDIUM TYPE: Floppy
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                ; LOCATION:
US-08-308-814-1
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US-08-455-001-1
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
PCT-0595-11869-1
Sequence 1, Application PC/TUS9511869
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION: EPH
TITLE OF INVENTION: Their
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
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255..324
                                                                                                                                                                                                                                                                                                                                       892..1809
                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                          MOLECULE TYPE: CDNA
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1..264
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LOCATION:
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US-08-455-001-1
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Search completed: July 13, 2002, 09:49:40 Job time: 4015 sec
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LENGTH: 314
          -09-609-324A-7
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                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISFRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMNUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7401
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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255..324
                                                                                                                                                                                                                                                                                                                                                                 892..1809
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FEATURE:
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                                                                                                                                                                                                                                       linear
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LOCATION:
FEATURE:
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LOCATION:
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                            GENERAL INFORMATION:
APPLICANT: CERRETIT, Douglas P.
APPLICANT: CERRETIT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
CURRENT PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1995-10-03
PRIOR FLILING DATE: 1995-10-03
PRIOR FLILING DATE: 1995-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                             Score 135.4; DB 1
Pred. No. 2.2e-19;
); Mismatches 66
; Sequence 7, Application US/09609324A; Patent No. RE37582
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ilarity 70.9%;
Conservative (
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; LOCATION: (2)..(313)
US-09-609-324A-7
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Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actacatct 428
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